

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 21:50:48 ; Search time 1396 Seconds
(without alignments)
869.345 Million cell updates/sec

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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1846492

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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32: em_htg_other:
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Pred. No. is the number of results predicted by chance to have a

SUMMARIES

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and is derived by analysis of the total score distribution.

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6	16	57.1	36	6	A66040	A66040 Sequence 22
7	16	57.1	36	6	AR08019	AR08019 Sequence
8	16	57.1	36	6	AR154830	AR154830 Sequence
9	16	57.1	36	6	AR343590	AR343590 Sequence
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11	15.2	54.3	65	6	AX486149	AX486149 Sequence
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13	15.2	54.3	84	9	AF357525	AF357525 Homo sapi
14	15.2	54.3	99	6	AX769938	AX769938 Sequence
15	15.2	54.3	99	6	AX769969	AX769969 Sequence
16	15.2	54.3	99	6	AX769972	AX769972 Sequence
17	15	53.6	24	6	AX039922	AX039922 Sequence
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19	15	53.6	43	6	I15393	I15393 Sequence 15
20	15	53.6	68	6	A39690	A39690 Sequence 3
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22	15	53.6	68	6	AR074511	AR074511 Sequence
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24	15	53.6	100	9	HUMPMC01	M83365 Human plasm
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41	14.6	52.1	98	6	AX797191	AX797191 Sequence
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DEFINITION Sequence 2 from patent US 5912168.
ACCESSION AR071972
VERSION AR071972.1 GI:7222860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Watson, J.D. and Rudert, F.
TITLE CD95 regulatory gene sequences
JOURNAL Patent: US 5912168-A 2 15-JUN-1999;
FEATURES Location/Qualifiers

linear PAT 18-FEB-2000

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date for 2/11 = 8/30/96

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ACCESSION AR071984
VERSION AR071984.1 GI:7222872
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 28)
AUTHORS Watson,J.D. and Rudert,F.
TITLE CD95 regulatory gene sequences
JOURNAL Patent: US 5912168-A 14 15-JUN-1999;
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DEFINITION Sequence 35 from patent US 5912168.
ACCESSION AR072005
VERSION AR072005.1 GI:7222893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 50)
AUTHORS Watson,J.D. and Rudert,F.
TITLE CD95 regulatory gene sequences
JOURNAL Patent: US 5912168-A 35 15-JUN-1999;
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DEFINITION Sequence 29 from patent US 5912168.
ACCESSION AR071999
VERSION AR071999.1 GI:7222887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
AUTHORS Watson,J.D. and Rudert,F.
TITLE CD95 regulatory gene sequences
JOURNAL Patent: US 5912168-A 29 15-JUN-1999;
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Db 10 GTCGGAAGTGCATCC 25

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LOCUS A62083 36 bp DNA linear PAT 09-MAR-1998
DEFINITION Sequence 18 from Patent WO9714719.
ACCESSION A62083
VERSION A62083.1 GI:3716134
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE
1
AUTHORS Davis,P.J., Van,D.L., Verhoeijen, Martine,E. and Wilson,S.
TITLE A BIFUNCTIONAL OR BIVALENT ANTIBODY FRAGMENT ANALOGUE
JOURNAL Patent: WO 9714719-A 18 24-APR-1997;
COMMENT UNILEVER NV (NL)
Other publication AU 6873396 970507.
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A66040
LOCUS A66040 36 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 22 from Patent WO9738102.
ACCESSION A66040
VERSION A66040.1 GI:4538027
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE
1 (bases 1 to 36)
AUTHORS Davis,P.J., Van,D.L. and Verhoeijen,M.E.

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TITLE MULTIVALENT AND MULTISPECIFIC ANTIGEN-BINDING PROTEIN
JOURNAL Patent: WO 9738102-A 22 16-OCT-1997;
UNILVER PLC (GB)
COMMENT Other publication AU 2507397 19971029.
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LOCUS Sequence 18 from patent US 5989830.
DEFINITION
ACCESSION AR088019
VERSION AR088019.1 GI:10014782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Davis,P.James., van der Logt,C.Paul.Erik., Verhoeven,M.Elisa. and Wilson,S.
TITLE Bifunctional or bivalent antibody fragment analogue
JOURNAL Patent: US 5989830-A 18 23-NOV-1999;
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RESULT 8
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LOCUS Sequence 22 from patent US 6239259.
DEFINITION
ACCESSION AR154830
VERSION AR154830.1 GI:15122883
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Davis,P.J., Logt van der,C.P. and Verhoeven,M.E.
TITLE Multivalent and multispecific antigen-binding protein
JOURNAL Patent: US 6239259-A 22 29-MAY-2001;
FEATURES Location/Qualifiers
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RESULT 9
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LOCUS Sequence 5 from patent US 6579842.
DEFINITION
ACCESSION AR343590
VERSION AR343590.1 GI:33739329
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Howell,S., Little,J., Van Der Logt,C.P. and Parry,N.J.
TITLE Method of treating fabrics
JOURNAL Patent: US 6579842-A 5 17-JUN-2003;
FEATURES Location/Qualifiers
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QY 5 GGAAGTCATCCAAATTCAGGTTTC 28
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Db 13 GGAGCTGCATGCAAAATTCATTTC 36

RESULT 10
AX613512/c 20 bp DNA linear PAT 17-FEB-2003
LOCUS Sequence 4537 from Patent WO20072882.
DEFINITION
ACCESSION AX613512
VERSION AX613512.1 GI:28408941
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 4537 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES Location/Qualifiers
source
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QY 8 ACTGCATCCAAATTCAG 24
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Db 20 ACTGCTTCCAAATTCAG 4

RESULT 11
AX486149 65 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 3449 from Patent WO02053728.
DEFINITION
ACCESSION AX486149

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VERSION      AX486149.1  GI:22320365
KEYWORDS
SOURCE       Candida albicans
ORGANISM     Candida albicans
REFERENCE    1 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
              1 Saccharomycetales; mitosporic Saccharomycetales; Candida.
AUTHORS      Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE        Gene disruption methodologies for drug target discovery
JOURNAL      Patent: WO 02053728-A 3449 11-JUL-2002;
              Elitra Pharmaceuticals, Inc. (US)
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LOCUS      AX386437      82 bp      DNA      linear      PAT 19-MAR-2002
DEFINITION Sequence 1365 from Patent WO0214500.
ACCESSION  AX386437
VERSION     AX386437.1  GI:19579567
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS      Escobedo,J., Garcia,P.D., Sudduth-Klinger,J., Reinhard,C.,
              Randazzo,F., Lamson,G., Scott,E.M., Zhang,G., Kassam,A., Pot,D. and
              Labat,I.
TITLE        Human genes and gene expression products
JOURNAL      Patent: WO 0214500-A 1365 21-FEB-2002;
              CHIRON CORPORATION (US); Hyseq Inc. (US)
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DB 26 ACCTGCTCTAAATTCAGGT 7

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LOCUS      AF357525      84 bp      mRNA      linear      PRI 11-JUN-2001
DEFINITION Homo sapiens Bcl-XL-binding protein c21 mRNA, partial cds.
ACCESSION  AF357525
VERSION     AF357525.1  GI:14335461
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 84)
AUTHORS      Hammond,P.W., Alpin,J., Rise,C.E., Wright,M. and Kreider,B.L.
TITLE        In vitro selection and characterization of Bcl-X(L)-binding
              proteins from a mix of tissue-specific mRNA display libraries
JOURNAL      J. Biol. Chem. 276 (24), 20898-20906 (2001)
MEDLINE      21293069
PUBMED       11293018
REFERENCE    2 (bases 1 to 84)
AUTHORS      Hammond,P.W., Alpin,J., Rise,C.E., Wright,M. and Kreider,B.L.
TITLE        Direct Submision
JOURNAL      Submitted (08-MAR-2001) Molecular Biology, Phyllos, Inc., 128 Spring
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LOCUS      AX769938      99 bp      DNA      linear      PAT 03-JUL-2003
DEFINITION Sequence 3 from Patent WO03016341.
ACCESSION  AX769938
VERSION     AX769938.1  GI:32437573
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS      Hubert,N. and Hentze,M.
TITLE        Regulation of iron uptake
JOURNAL      Patent: WO 03016341-A 3 27-FEB-2003;
              European Molecular Biology Laboratory (DE)
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ACCESSION  AX769969
VERSION     AX769969.1  GI:32437600
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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KEYWORDS Homo sapiens (human)
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Hubert, N. and Hentze, M.
 TITLE Regulation of iron uptake
 JOURNAL Patent: WO 03016341-A 34 27-FEB-2003;
 European Molecular Biology Laboratory (DE)
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 Job time : 1398 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 21:27:22 ; Search time 231 Seconds
(without alignments)
514.933 Million cell updates/sec

Title: US-10-028-415-2
Perfect score: 28
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SUMMARIES

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20	15.2	54.3	66	2 AAT21089	AAT21089 Human gen
21	15.2	54.3	82	6 ABN61398	ABN61398 Human can
22	15.2	54.3	84	7 ABT14837	ABT14837 Human Bcl
23	15.2	54.3	96	2 AAT47779	AAT47779 Polyclona

C 24	15.2	54.3	99	7	ABQ80179	Abq80179 Human DMT
C 25	15.2	54.3	100	7	ACD69282	AcD69282 E. coli K
C 26	15	53.6	24	3	AAC67600	Aac67600 Alzheimer
C 27	15	53.6	24	9	ADD43523	Add43523 Human mit
C 28	15	53.6	28	3	AAAI5192	Aaai5192 PCR prime
C 29	15	53.6	33	6	ABL41320	Adl41320 Human GTP
C 30	15	53.6	43	2	AAQ62546	Aaq62546 Probe spe
C 31	15	53.6	68	2	AAQ71837	Aaq71837 pBROC531
C 32	15	53.6	68	2	AAQ71836	Aaq71836 pBROC531
C 33	15	53.6	68	2	AAT18305	Aat18305 Nucleotid
C 34	15	53.6	68	2	AAT18305	Aat18305 Nucleotid
C 35	15	53.6	83	2	AAV73250	Aav73250 C. utilis
C 36	14.8	52.9	27	2	AAZ30800	Aaz30800 SCBV viru
C 37	14.8	52.9	60	6	ABN46107	Abn46107 Human spl
C 38	14.8	52.9	60	6	ABN47820	Abn47820 Human spl
C 39	14.8	52.9	60	6	ABN46731	Abn46731 Human spl
C 40	14.8	52.9	90	6	ABN69180	Abn69180 Streptoco
C 41	14.8	52.9	100	7	ACD80222	AcD80222 E. coli K
C 42	14.6	52.1	41	6	ABZ48776	Abz48776 Human ald
C 43	14.6	52.1	41	6	ABZ46265	Abz46265 Human ald
C 44	14.6	52.1	50	4	AAL31606	Aal31606 Human SNP
C 45	14.6	52.1	50	4	AAL31607	Aal31607 Human SNP

ALIGNMENTS

RESULT 1
AAV20897
ID AAV20897 standard; DNA; 28 BP.
XX AC AAV20897;
XX DT 23-JUL-1998 (first entry)
XX DE CD95 regulatory region.
XX KW CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;
XX KW cancer; viral infection; neurodegeneration; autoimmune disease;
XX KW Gene therapy; transcription factor; ss.
XX OS Homo sapiens.
XX PN WO9808965-A2.
XX PD 05-MAR-1998.
XX PF 29-AUG-1997; 97WO-NZ000107.
XX PR 30-AUG-1996; 96US-00713557.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Watson JD, Rudert F;
XX WPI; 1998-179445/16.
XX New regulatory regions from the CD95 gene and transcription factors that
XX interact with them - for control of apoptosis, e.g. in treatment of
XX cancer, viral infection, neurodegeneration and autoimmune disease.
XX Claim 1; Page 36; 60pp; English.
XX This sequence represents a regulatory region from the CD95 gene, and is a
XX nucleic acid of the invention. The regulatory regions (silencers or
XX enhancers) are involved in apoptosis, i.e. inhibition of CD95 expression
XX will inhibit apoptosis. Regulation of apoptosis is useful in treatment of
XX cancer, (retroviral) infection, neurodegeneration and autoimmune disease,
XX e.g. by gene therapy for expressing transcription factors or expression
XX of antisense sequences to inhibit transcription factor production. The
XX regulatory nucleic acids and transcription factors are also useful for
XX studying regulation of CD95 in vitro or in vivo, to screen for modulators
XX and as probes to isolate related genes

```

XX SQ Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAACCTGCATCCAAATTCAGGTTTC 28
Db 1 GTCGGAACCTGCATCCAAATTCAGGTTTC 28

RESULT 2
AAV23143/c
ID AAV23143 standard; DNA; 28 BP.
XX AC AAV23143;
XX AC AAV23143;
XX DT 23-JUL-1998 (first entry)
XX DE CD95 regulatory region.
XX KW CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;
XX KW cancer; viral infection; neurodegeneration; autoimmune disease;
XX KW gene therapy; transcription factor; ss.
XX OS Homo sapiens.
XX PN WO9808965-A2.
XX PD 05-MAR-1998.
XX PF 29-AUG-1997; 97WO-NZ000107.
XX PR 30-AUG-1996; 96US-00713557.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Watson JD, Rudert F;
XX WPI; 1998-179445/16.
XX PT New regulatory regions from the CD95 gene and transcription factors that
XX PT interact with them - for control of apoptosis, e.g. in treatment of
XX PT cancer, viral infection, neurodegeneration and autoimmune disease.
XX PS Claim 1; Page 38; 60pp; English.
XX CC This sequence represents a regulatory region from the CD95 gene, and is a
XX CC nucleic acid of the invention. The regulatory regions (silencers or
XX CC enhancers) are involved in apoptosis, i.e. inhibition of CD95 expression
XX CC will inhibit apoptosis. Regulation of apoptosis is useful in treatment of
XX CC cancer, (retroviral infection, neurodegeneration and autoimmune disease,
XX CC e.g. by gene therapy for expressing transcription factors or expression
XX CC of antisense sequences to inhibit transcription factor production. The
XX CC regulatory nucleic acids and transcription factors are also useful for
XX CC studying regulation of CD95 in vitro or in vivo, to screen for modulators
XX CC and as probes to isolate related genes
XX SQ Sequence 28 BP; 8 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAACCTGCATCCAAATTCAGGTTTC 28
Db 28 GTCGGAACCTGCATCCAAATTCAGGTTTC 1

RESULT 3
ABK88709/c
ID ABK88709 standard; DNA; 28 BP.

```

```

XX AC ABK88709;
XX DT 07-OCT-2002 (first entry)
XX DE Human CD95 gene transcription silencer probe #1.
XX KW Human; apoptotic cell death; proteinaceous transcription factor;
XX KW regulation of gene transcription; apoptosis; p53; CD95; TRA;
XX KW transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;
XX KW tumour cell; embryonic cell; nervous system; intracellular pathogen;
XX KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;
XX KW immune system dysfunction; anti-tumour; cytostatic; hCD95;
XX KW transcription silencer region; probe; ss.
XX OS Homo sapiens.
XX PN WO200244363-A1.
XX PD 06-JUN-2002.
XX PF 28-NOV-2001; 2001WO-NZ000287.
XX PR 28-NOV-2000; 2000US-00724809.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Lasham A, Watson JD;
XX WPI; 2002-557540/59.
XX PT Modulating p53-mediated apoptotic cell death in a population of cells, by
XX PT modulating the amount of a transcriptional regulator of apoptosis
XX PT available to bind to a target polynucleotide in the cells.
XX PS Example 1; Page 54; 62pp; English.
XX CC The present invention relates to methods for modulating apoptotic cell
XX CC death using proteinaceous transcription factors that regulate the
XX CC transcription of genes encoding proteins involved in apoptosis (e.g. CD95
XX CC and p53). The methods involve modulating the amount of a transcriptional
XX CC regulator of apoptosis (TRA) available to bind to a target polynucleotide
XX CC in the cells, where TRA is a member of the Y-box nucleic acid binding
XX CC family of polypeptides (e.g. YB-1). The methods of the invention are
XX CC useful for modulating apoptotic cell death in a population of cells,
XX CC where the cells are selected from tumour cells, cells of the immune
XX CC system, embryonic cells, cells of the nervous system, or cells infected
XX CC with intracellular pathogens. The methods are also useful for increasing
XX CC the sensitivity of tumour cells to a DNA-damaging agent, and for
XX CC increasing sensitivity to apoptosis in a population of cells harbouring
XX CC intracellular pathogens. The methods are useful for screening an
XX CC apoptosis modulatory agent that modulates the binding of TRA. The methods
XX CC for regulating apoptosis can be used therapeutically and prophylactically
XX CC for various disorders such as cancer, viral and retroviral infections,
XX CC neurodegenerative disorders, and immune system dysfunction. The present
XX CC sequence represents a human CD95 (hCD95) gene transcription silencer
XX CC probe
XX SQ Sequence 28 BP; 8 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAACCTGCATCCAAATTCAGGTTTC 28
Db 28 GTCGGAACCTGCATCCAAATTCAGGTTTC 1

RESULT 4
ABK88700
ID ABK88700 standard; DNA; 28 BP.
XX

```

AC ABK8700;
XX
XX
DT 07-OCT-2002 (first entry)
XX
XX
DE Transcription silencer region (S1) of human CD95 gene.
XX
XX
DE Human; apoptotic cell death; proteinaceous transcription factor;
KW regulation of gene transcription; apoptosis; p53; CD95; TRA;
KW transcriptional regulator of apoptosis; I-box family; YB-1; cancer;
KW tumour cell; embryonic cell; nervous system; intracellular pathogen;
KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;
KW immune system dysfunction; anti-tumour; cytostatic; S1; hCD95;
KW transcription silencer region; ds.
XX
XX
OS Homo sapiens.
XX
XX WO200244363-A1.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-NZ000287.
XX
XX 28-NOV-2000; 2000US-00724809.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Lasham A, Watson JD;
XX
XX WPI; 2002-557540/59.
XX
XX Modulating p53-mediated apoptotic cell death in a population of cells, by
PT modulating the amount of a transcriptional regulator of apoptosis
PT available to bind to a target polynucleotide in the cells.
XX
XX Example 1; Page 53; 62pp; English.
XX
XX The present invention relates to methods for modulating apoptotic cell
CC death using proteinaceous transcription factors that regulate the
CC transcription of genes encoding proteins involved in apoptosis (e.g. CD95
CC and p53). The methods involve modulating the amount of a transcriptional
CC regulator of apoptosis (TRA) available to bind to a target polynucleotide
CC in the cells, where TRA is a member of the Y-box nucleic acid binding
CC family of polypeptides (e.g. YB-1). The methods of the invention are
CC useful for modulating apoptotic cell death in a population of cells,
CC where the cells are selected from tumour cells, cells of the immune
CC system, embryonic cells, cells of the nervous system, or cells infected
CC with intracellular pathogens. The methods are also useful for increasing
CC the sensitivity of tumour cells to a DNA-damaging agent, and for
CC increasing sensitivity to apoptosis in a population of cells harbouring
CC intracellular pathogens. The methods are useful for screening an
CC apoptosis modulatory agent that modulates the binding of TRA. The methods
CC for regulating apoptosis can be used therapeutically and prophylactically
CC for various disorders such as cancer, viral and retroviral infections,
CC neurodegenerative disorders, and immune system dysfunction. The present
CC sequence represents the transcription silencer region (S1) of the human
XX CD95 (hCD95) gene
XX
SQ Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAACCTGCATCCAAATTCAGGTTTC 28
Db 1 GTCTGGAACCTGCATCCAAATTCAGGTTTC 28

RESULT 5
AAV23172
ID AAV23172 standard; DNA; 50 BP.
XX
XX AAV23172;
AC

XX 23-JUL-1998 (first entry)
XX
XX CD95 enhancer binding site.
XX
XX CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;
KW cancer; viral infection; neurodegeneration; autoimmune disease;
KW gene therapy; transcription factor; ss.
XX
XX Homo sapiens.
XX
XX WO9808965-A2.
XX
XX 05-MAR-1998.
XX
XX 29-AUG-1997; 97WO-NZ000107.
XX
XX 30-AUG-1996; 96US-00713557.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Rudert F;
XX
XX WPI; 1998-179445/16.
XX
XX New regulatory regions from the CD95 gene and transcription factors that
PT interact with them - for control of apoptosis, e.g. in treatment of
PT cancer, viral infection, neurodegeneration and autoimmune disease.
XX
XX Disclosure; Page 43; 60pp; English.
XX
XX This sequence represents a regulatory region from the CD95 gene, and is a
CC nucleic acid of the invention. The regulatory regions (silencers or
CC enhancers) are involved in apoptosis, i.e. inhibition of CD95 expression
CC will inhibit apoptosis. Regulation of apoptosis is useful in treatment of
CC cancer, (retro)viral infection, neurodegeneration and autoimmune disease,
CC e.g. by gene therapy for expressing transcription factors or expression
CC of antisense sequences to inhibit transcription factor production. The
CC regulatory nucleic acids and transcription factors are also useful for
CC studying regulation of CD95 in vitro or in vivo, to screen for modulators
XX and as probes to isolate related genes
XX
SQ Sequence 50 BP; 16 A; 10 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAACCTGCATCCAAATTCAGGTTTC 28
Db 1 GTCTGGAACCTGCATCCAAATTCAGGTTTC 28

RESULT 6
ABN55985/C
ID ABN55985 standard; DNA; 65 BP.
XX
XX AC ABN55985;
XX
XX 15-JUL-2002 (first entry)
XX
XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:28733.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Mus musculus.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB001903.
XX
XX Pf

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XX 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 28733; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
XX transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridising selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The
XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterising the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a particular
XX biological or pathological state, and so allowing the detection of tissue
XX - and pathology-specific genes such as those genes only expressed in
XX specific tissue under a specific pathological condition; to detect
XX developmental specific genes; and to detect RNA transcripts and splice
XX variants of a transcriptome of a patient suffering from a particular
XX disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
XX rats, humans and mice, which are used in the exemplification of the
XX present invention. N.B. The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 65 BP; 18 A; 16 C; 17 G; 14 T; 0 U; 0 Other;
XX
Query Match 61.4%; Score 17.2; DB 6; Length 65;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CTGGAACCTGCATCCAAATTCAG 24
DB 61 CTGCACCTGCAGCAAAATTCAG 40
RESULT 7
ABN37069/c
ID ABN37069 standard; DNA; 60 BP.
XX AC ABN37069;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:9817.
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX Homo sapiens.
XX
XX WC200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB001903.
XX

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PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 9817; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
XX transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridising selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The
XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterising the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a particular
XX biological or pathological state, and so allowing the detection of tissue
XX - and pathology-specific genes such as those genes only expressed in
XX specific tissue under a specific pathological condition; to detect
XX developmental specific genes; and to detect RNA transcripts and splice
XX variants of a transcriptome of a patient suffering from a particular
XX disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
XX rats, humans and mice, which are used in the exemplification of the
XX present invention. N.B. The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 60 BP; 15 A; 14 C; 18 G; 13 T; 0 U; 0 Other;
XX
Query Match 59.3%; Score 16.6; DB 6; Length 60;
Best Local Similarity 82.6%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CTGGAACCTGCATCCAAATTCAGG 25
DB 35 CTGCTCTCGTCCAAAGTCAGG 13
RESULT 8
ACD75131/c
ID ACD75131 standard; DNA; 100 BP.
XX AC ACD75131;
XX
XX 18-SEP-2003 (first entry)
XX
XX E. coli K12 MG1655 biochip probe SEQ ID 6407.
XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX Escherichia coli.
XX
XX EPI260592-A1.
XX
XX 27-NOV-2002.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX

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PA (MWGE-) MWG-BIOTECH AG.
 XX
 PI Donner H, Drescher B, Huber A, Weber J;
 XX WPI; 2003-241155/24.
 XX Biochip containing probes complementary with open reading frames in
 PT Escherichia coli K12, useful for detecting gene expression and expression
 PT patterns.
 XX
 PS Claim 3; Page 1002; 2004pp; German.
 XX This invention describes a novel biochip comprising probe spots, each
 CC containing many identical probes. The probes are nucleotide sequences of
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
 CC least one includes a segment of at least 20 bases identical with, or
 CC complementary to, a segment of an open reading frame (orf) of Escherichia
 CC coli K12. The biochip is used for specific detection of gene expression
 CC in K12 and for determining the gene expression pattern, e.g. for
 CC diagnostic determination of which E. coli strains are present in the gut,
 CC and to determine the effects of e.g. growth media on gene expression. The
 CC biochip provides as comprehensive as possible detection of the K12
 CC genome, with simultaneous analysis of many different genes with a single
 CC device, and comparison of gene expression between K12 and its mutants or
 CC other E. coli strains in a single experiment. Apart from qualitative and
 CC quantitative information about gene expression, it also allows
 CC measurements of population densities for the various strains. The use of
 CC synthetic oligonucleotides for preparation of probes allows free
 CC variation in probe length and ensures high purity (and thus selectivity,
 CC reactivity and reproducibility); also synthetic probes are generally
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
 CC ACD81540 represent oligonucleotide probes used with the biochip described
 CC in the invention
 XX
 SQ Sequence 100 BP; 19 A; 20 C; 31 G; 30 T; 0 U; 0 Other;
 Query Match 58.6%; Score 16.4; DB 7; Length 100;
 Best Local Similarity 76.9%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 3 CTGGAACTGCATCCAAATCAGGTC 28
 DB 88 CCGGAACGGCATCCCACTTCAGATC 63
 RESULT 9
 AAV23161
 ID AAV23161 standard; DNA; 25 BP.
 AC AAV23161;
 DT 23-JUL-1998 (first entry)
 DE Primer -1035/-1/CAT for human CD95 gene.
 XX
 KW CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;
 KW cancer; viral infection; neurodegeneration; autoimmune disease; human;
 KW gene therapy; transcription factor; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN WO9808965-A2.
 XX
 PD 05-MAR-1998.
 XX
 PF 29-AUG-1997; 97WO-NZ000107.
 XX
 PR 30-AUG-1996; 96US-00713557.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 PI Watson JD, Rudert F;
 WPI; 1998-179445/16.
 New regulatory regions from the CD95 gene and transcription factors that
 interact with them - for control of apoptosis, e.g. in treatment of
 cancer, viral infection, neurodegeneration and autoimmune disease.
 Disclosure; Page 42; 60pp; English.
 This sequence is a primer for the CD95 gene, and is used to isolate the
 regulatory nucleic acids of the invention. The regulatory regions
 (silencers or enhancers) are involved in apoptosis, e.g. inhibition of
 CD95 expression will inhibit apoptosis. Regulation of apoptosis is useful
 in treatment of cancer, (retro)viral infection, neurodegeneration and
 autoimmune disease, e.g. by gene therapy for expressing transcription
 factors or expression of antisense sequences to inhibit transcription
 factor production. The regulatory nucleic acids and transcription factors
 are also useful for studying regulation of CD95 in vitro or in vivo, to
 screen for modulators and as probes to isolate related genes
 Sequence 25 BP; 5 A; 7 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 57.1%; Score 16; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCTGGAATCCTCATCC 16
 DB 10 GTCTGGAATCCTCATCC 25
 RESULT 10
 AAT66152
 ID AAT66152 standard; DNA; 36 BP.
 AC AAT66152;
 DT 14-JUL-1997 (first entry)
 DE Primer DBL.5 used in vector pGOSA.E construction.
 XX
 KW Bispecific antibody; bivalent antibody; double head;
 KW antibody engineering; glucose oxidase; Streptococcus sanguis; GOSA.E;
 KW vector; polymerase chain reaction; PCR; primer; ss.
 XX
 OS Synthetic.
 XX WO9714719-A1.
 PN
 DT 24-APR-1997.
 DE
 PF 14-AUG-1996; 96WO-EP003605.
 XX
 PR 16-OCT-1995; 95EP-00307332.
 XX
 PA (UNIL) UNILEVER NV.
 PA (UNIL) UNILEVER PLC.
 XX
 PI Davis PJ, Van Der Logt CPE, Verhoeijen ME, Wilson S;
 WPI; 1997-245049/22.
 Bi-specific or bivalent antibody fragment analogues comprise complex of
 two polypeptide chains containing respectively two heavy and two light
 chain variable domains - useful therapeutically, in immunoassays, for
 purification etc.
 Example 1; Page 18; 121pp; English.
 PCR primers (AAT66148-63) were utilised in the construction of 'double
 head' expression vector pGOSA.E (see also AAT66147) which encodes a
 bispecific antibody (see also AAW09818-20) for glucose oxidase and
 Streptococcus sanguis. The primers were used to generate restriction

CC sites to facilitate the cloning of DNA fragments utilised in vector
 CC construction. Primer DBL.5 (AA766152) contg. an NheI site was designed to
 CC match the sequence upstream of the ribosome binding site of VL.4715 in
 CC Fv4715 and to introduce an NheI site
 XX
 SQ Sequence 36 BP; 11 A; 7 C; 7 G; 11 T; 0 U; 0 Other;

Query Match 57.1%; Score 16; DB 2; Length 36;
 Best Local Similarity 79.2%; Pred. No. 1.9e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGAAGTGCATCCAAATTCAGTTTC 28
 ||| ||||| ||||| ||||| |||||
 Db 13 GGAGCTGCATCCAAATTCATTTTC 36

RESULT 11

ID AAT94605 standard; DNA; 36 BP.

AC AAT94605;

DT 24-APR-1998 (first entry)

DE Construction of trispecific pSV constructs using primer DBL.10.

XX Multivalent antigen binding protein; variable domain; binding site;
 KW diagnosis; therapy; medicine; immunoassay; target; trispecific;
 KW pSV construct; PCR primer; ss.
 XX Synthetic.

XX WO9738102-A1.

XX 16-OCT-1997.

XX 26-MAR-1997; 97WO-EF001609.

XX 04-APR-1996; 96EP-00302412.

XX (UNIL) UNILEVER PLC.

XX (UNIL) UNILEVER NV.

XX Davis PJ, Van Der Logt CPE, Verhoeven ME;

XX WPI; 1997-512719/47.

XX Multivalent antigen binding protein - comprises antibody variable
 PT domains, linked by their association, where each associated variable
 PT domain pair forms an antigen binding site.
 XX Disclosure; Page 41; 100pp; English.

XX This PCR primer is used in the construction of the trispecific pSV
 CC constructs which are used to construct a novel multivalent antigen
 CC binding protein. This novel protein comprises 2 polypeptides, each
 CC comprising, in series, 3 or more variable domains of an antibody heavy or
 CC light chain respectively, which are linked by association of the
 CC respective heavy and light chain variable domains, where each associated
 CC variable domain pair forms an antigen binding site. The multivalent
 CC antigen binding protein can be used in medicine, diagnosis, therapy, an
 CC immunoassay method or for purification. It may be used in targeting a
 CC tumour cell with natural killer cells and cytotoxic agents. It may be
 CC used to target cell killing enzymes, e.g. oxidases and peroxidases, to a
 CC species with which is an antigenic component of a dental plaque, such as
 CC S. sanguis or S. mutans. The antigen binding protein may conveniently be
 CC purified straight from the supernatant using conventional purification
 CC techniques. As the protein is self-assembling, there is no need to purify
 CC individual subunits prior to coupling as in existing techniques

SQ .Sequence 36 BP; 11 A; 7 C; 7 G; 11 T; 0 U; 0 Other;

Query Match 57.1%; Score 16; DB 2; Length 36;

Best Local Similarity 79.2%; Pred. No. 1.9e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGAAGTGCATCCAAATTCAGTTTC 28
 ||| ||||| ||||| ||||| |||||
 Db 13 GGAGCTGCATCCAAATTCATTTTC 36

RESULT 12

AAAL53506 standard; DNA; 36 BP.

XX AAAL53506;

DT 30-JAN-2003 (first entry)

DE Serotonin receptor internal oligo probe SEQ ID No 10.

XX Immunomodulator; antirheumatic; antiarthritic; immunosuppressive;
 KW haemostatic; antiinflammatory; antiulcer; neuroprotective; antithyroid;
 KW antidiabetic; dermatological; antipsoriatic; gynaecological; vasotropic;
 KW anti-HIV; immune response; inhibitor; serotonin; serotonin receptor;
 KW CD-4; CD-8; T cell; B cell; autoimmune disease; fulminant AIDS;
 KW serotonin receptor oligonucleotide probe; ss.

XX Unidentified.

XX WO200278643-A2.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-US009993.

XX 30-MAR-2001; 2001US-0280296P.

XX 25-OCT-2001; 2001US-0345295P.

XX 31-JAN-2002; 2002US-0353883P.

XX (PHIL-) PHILADELPHIA HEALTH & EDUCATION CORP.

XX Jameson BA, Tretiakova AS, Albert R, Davidson HC;

XX WPI; 2003-040619/03.

XX Modulating immune response in mammal in treatment of e.g. multiple
 PT sclerosis, myasthenia gravis, chronic neutropenia, Crohn's disease,
 PT endometriosis, involves administering inhibitor of interaction of
 PT serotonin with serotonin receptor.

XX Example 2; Page 21; 172pp; English.

XX The invention relates to a discovery that modulating an immune response
 CC in a mammal involves administering an inhibitor of the interaction of
 CC serotonin with a serotonin receptor. The invention is useful for
 CC modulating (e.g. inhibiting) an immune response (such as CD-4 or CD-8
 CC dependent immune response); for inhibiting an immune reaction or response
 CC mediated by activation of serotonin receptor on an immune cell (such as T
 CC cell and B cell) due to the activation of the serotonin receptor on the
 CC cell; for modulating an immune response of an autoimmune disease (such as
 CC myasthenia gravis, idiopathic inflammatory myopathy, chronic neutropenia,
 CC rheumatoid arthritis, idiopathic thrombocytopenia purpura, autoimmune
 CC haematolytic syndromes, antiphospholipid antibody syndromes, inflammatory
 CC bowel disease, Crohn's disease, ulcerative colitis, myocarditis, Guillain
 CC Barre syndrome, vasculitis, multiple sclerosis, neuromyelitis optica
 CC (Devic's syndrome), lymphocytic hypophysitis, Grave's disease, Addison's
 CC disease, hypoparathyroidism, type I diabetes, systemic lupus erythematus,
 CC pemphigus vulgaris, bullous pemphigoid, psoriasis, psoriatic arthritis,
 CC endometriosis, autoimmune orchitis, autoimmune erectile dysfunction,
 CC sarcoidosis, Wegener's granulomatosis, autoimmune deafness, Sjogren's
 CC disease, autoimmune uveoretinitis, interstitial cystitis, Goodpasture's
 CC syndrome, and fibromyalgia); for inhibiting a secondary immune response,
 CC in a mammal (preferably a human); and for inducing apoptosis or death in
 CC a cell or affecting a cell cycle process in a cell expressing a serotonin
 CC receptor by inhibiting transmission of a serotonin signal via a serotonin

CC receptor. The invention is also useful for treating fulminant AIDS. This
 CC polynucleotide sequence represents a serotonin receptor oligonucleotide
 CC probe relating to the invention

XX Sequence 36 BP; 12 A; 13 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 57.1%; Score 16; DB 7; Length 36;
 Best Local Similarity 79.2%; Pred. No. 1.9e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAACCTGCATCCAAATTCAGG 25
 |||||
 Db 10 TCAGCAACTACCTCCAACTCAGG 33

RESULT 13

ABZ04805
 ID ABZ04805 standard; DNA; 50 BP.

XX AC ABZ04805;

XX 09-JAN-2003 (first entry)

XX Human leukocyte gene expression profiling probe SEQ ID NO 4796.

XX T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.

XX Homo sapiens.

XX WO200257414-A2.

XX 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.

XX 20-OCT-2000; 2000US-0241994P.

XX 08-JUN-2001; 2001US-0296764P.

XX (BIOC-) BIOCARDIA INC.

XX Wohlgemuth J, Fry X, Marcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quertemous T, Johnson F;

XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 481; Opp; English.

XX The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX Sequence 50 BP; 15 A; 13 C; 7 G; 15 T; 0 U; 0 Other;

Query Match 56.4%; Score 15.8; DB 6; Length 50;
 Best Local Similarity 74.1%; Pred. No. 2.4e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCTGGAACCTGCATCCAAATTCAGGTTTC 28
 |||||
 Db 24 TCTGGTACTAGCTACAAATTCGGTTTC 50

RESULT 14

ABN39933/c
 ID ABN39933 standard; DNA; 60 BP.

XX AC ABN39933;

XX 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:12681.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB001903.

XX 28-JUL-2000; 2000US-0221607P.

XX 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 PI WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.

XX Example 1; SEQ ID NO 12681; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 60 BP; 11 A; 19 C; 16 G; 14 T; 0 U; 0 Other;

Query Match 55.7%; Score 15.6; DB 6; Length 60;
 Best Local Similarity 81.8%; Pred. No. 3.1e+03;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CTGGAACCTGCATCCAAATTCAG 24

DB 46 CAGGAAGTGCACCCAGATTCCG 25

RESULT 15
ABN28998

ID ABN28998 standard; DNA; 65 BP.

XX AC ABN28998;

XX DT 15-JUL-2002 (first entry)

XX DE Rat spliced transcript detection oligonucleotide SEQ ID NO:1746.

XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;

XX KW splice variant; transcriptome; oligonucleotide library; ss.

XX OS Rattus norvegicus.

XX PN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB001903.

XX PR 28-JUL-2000; 2000US-0221607P.

XX PR 02-MAY-2001; 2001US-0287724P.

XX PA (COMP-) COMPUGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI; 2002-257383/30.

XX PT New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes.

XX PS Example 1; SEQ ID NO 1746; 47pp; English.

XX CC The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini-libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN2753 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 65 BP; 15 A; 17 C; 19 G; 14 T; 0 U; 0 Other;

Query Match 55.7%; Score 15.6; DB 6; Length 65;
Best Local Similarity 81.8%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGGAAGTGCACCCAGATTCCG 22

DB 23 GGCTGGAAGTGAAGCCACATTC 44

Search completed: September 1, 2004, 22:43:28
Job time : 234 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 21:55:47 ; Search time 49 Seconds
(without alignments)
317.115 Million cell updates/sec

Title: US-10-028-415-2

Perfect score: 28
Sequence: 1 gctggaactgcatacaattcagggttc 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 939290

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	2	US-08-713-557B-2
2	28	100.0	28	2	US-08-713-557B-14
3	28	100.0	50	2	US-08-713-557B-35
4	16	57.1	25	2	US-08-713-557B-29
5	16	57.1	36	2	US-08-860-174A-18
6	16	57.1	36	3	US-09-171-025-22
7	16	57.1	36	4	US-09-742-693-5
8	15	54.3	40	5	PCT-US95-11405-20
9	15	53.6	43	1	US-07-938-084-15
10	15	53.6	68	2	US-08-459-135A-3
11	15	53.6	68	2	US-08-459-135A-4
12	15	53.6	68	3	US-08-495-559-3
13	15	53.6	68	3	US-08-495-559-4
14	14.6	52.1	58	3	US-09-140-466-9
15	14.6	52.1	58	3	US-09-140-466-10
16	14.6	52.1	59	1	US-08-313-127A-2
17	14.6	52.1	66	1	US-08-313-127A-1
18	14.4	51.4	47	4	US-09-422-978-3861
19	14.4	51.4	59	4	US-08-956-171E-5133
20	14.4	51.4	80	3	US-09-077-690-3
21	14.2	50.7	31	1	US-08-347-826A-6
22	14.2	50.7	39	1	US-08-644-864B-35
23	14.2	50.7	39	2	US-08-761-277A-35
24	14	50.0	14	2	US-08-713-557B-12
25	14	50.0	14	2	US-08-713-557B-13
26	14	50.0	14	2	US-08-713-557B-15
27	14	50.0	14	2	US-08-713-557B-16

28 14 50.0 14 2 US-08-713-557B-17 Sequence 17, Appl
C 29 14 50.0 14 2 US-08-713-557B-18 Sequence 18, Appl
C 30 14 50.0 29 2 US-08-607-631-4 Sequence 4, Appl
C 31 14 50.0 32 1 US-08-068-945A-39 Sequence 39, Appl
C 32 14 50.0 32 1 US-08-442-806-39 Sequence 39, Appl
C 33 14 50.0 61 3 US-09-275-850-70 Sequence 70, Appl
C 34 14 50.0 61 4 US-09-254-968-132 Sequence 132, Appl
C 35 13.8 49.3 29 2 US-08-481-793-5 Sequence 5, Appl
C 36 13.8 49.3 29 2 US-08-354-326-5 Sequence 5, Appl
C 37 13.8 49.3 29 5 PCT-US95-07068-5 Sequence 5, Appl
C 38 13.8 49.3 30 3 US-09-091-219-17 Sequence 17, Appl
C 39 13.8 49.3 30 4 US-09-660-541-17 Sequence 17, Appl
C 40 13.8 49.3 37 3 US-08-961-083-257 Sequence 257, Appl
C 41 13.8 49.3 37 4 US-09-536-784-257 Sequence 257, Appl
C 42 13.8 49.3 45 4 US-09-314-701-64 Sequence 64, Appl
C 43 13.8 49.3 47 4 US-09-422-978-1620 Sequence 1620, Ap
C 44 13.8 49.3 47 4 US-09-422-978-2877 Sequence 2877, Ap
C 45 13.6 48.6 20 3 US-09-226-568-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-713-557B-2
; Sequence 2, Application US/08713557B
; Patent No. 5912168
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Rudert, Fritz
; TITLE OF INVENTION: CD95 REGULATORY GENE SEQUENCES
; TITLE OF INVENTION: AND TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,557B
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Speckman, Ann W
; REGISTRATION NUMBER: 31,881
; REFERENCE/DOCKET NUMBER: 11000.1004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-713-557B-2

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGAAGTGCATCCAAATTCAGGTTC 28

Db 1 GTCTGGAAGTGCATCCAAATTCAGGTTTC 28

RESULT 2

US-08-713-557B-14/c
; Sequence 14, Application US/08713557B
; Patent No. 5912168
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Rudert, Fritz
; TITLE OF INVENTION: CD95 REGULATORY GENE SEQUENCES
; TITLE OF INVENTION: AND TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08713.557B

FILING DATE: 30-AUG-1996

CLASSIFICATION: 536

PRIOR APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Speckman, Ann W

REGISTRATION NUMBER: 31,881

REFERENCE/DOCKET NUMBER: 11000.1004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-713-557B-14

Query Match 100.0%; Score 28; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00026;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTGCATCCAAATTCAGGTTTC 28

Db 28 GTCTGGAAGTGCATCCAAATTCAGGTTTC 1

RESULT 3

US-08-713-557B-35

; Sequence 35, Application US/08713557B

; Patent No. 5912168

; GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Rudert, Fritz

TITLE OF INVENTION: CD95 REGULATORY GENE SEQUENCES

TITLE OF INVENTION: AND TRANSCRIPTION FACTORS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08713.557B
FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Speckman, Ann W
REGISTRATION NUMBER: 31,881
REFERENCE/DOCKET NUMBER: 11000.1004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-713-557B-35

Query Match 100.0%; Score 28; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.0003;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTGCATCCAAATTCAGGTTTC 28

Db 1 GTCTGGAAGTGCATCCAAATTCAGGTTTC 28

RESULT 4

US-08-713-557B-29

; Sequence 29, Application US/08713557B

; Patent No. 5912168

; GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Rudert, Fritz

TITLE OF INVENTION: CD95 REGULATORY GENE SEQUENCES

TITLE OF INVENTION: AND TRANSCRIPTION FACTORS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08713.557B

FILING DATE: 30-AUG-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Speckman, Ann W

REGISTRATION NUMBER: 31,881

REFERENCE/DOCKET NUMBER: 11000.1004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-713-557B-29

Query Match 57.1%; Score 16; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTCATCC 16
|||||
DB 10 GTCTGGAAGTCATCC 25

RESULT 5

US-08-860-174A-18
Sequence 18, Application US/08860174A
Patent No. 5989830

GENERAL INFORMATION:

APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
STREET: 9th Floor, East Tower
CITY: WASHINGTON, D.C.
STATE:

COUNTRY: UNITED STATES

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

IMMEDIATE SOURCE:

CLONE: primer DBL.5

US-08-860-174A-18

Query Match 57.1%; Score 16; DB 2; Length 36;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGAACTGCATCCAAATTCAGGTTTC 28
|||||
DB 13 GGAGCTGCATGCAAAATTCATTTC 36

RESULT 6

US-09-171-025-22

Sequence 22, Application US/09171025
Patent No. 6239259

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Multivalent and multispecific antigen-binding
TITLE OF INVENTION: protein
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,025
FILING DATE:

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
IMMEDIATE SOURCE:
CLONE: primer DBL.10

US-09-171-025-22

Query Match 57.1%; Score 16; DB 3; Length 36;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGAACTGCATCCAAATTCAGGTTTC 28
|||||
DB 13 GGAGCTGCATGCAAAATTCATTTC 36

RESULT 7

US-09-742-693-5

Sequence 5, Application US/09742693
Patent No. 6579842

GENERAL INFORMATION:

APPLICANT: HOWELL, Steven
APPLICANT: LITTLE, Julie C.
APPLICANT: VAN DER LOGT, Cornelis P.
APPLICANT: PAREY, Neil J.
TITLE OF INVENTION: METHOD OF TREATING FABRICS
FILE REFERENCE: C7536 (V)
CURRENT APPLICATION NUMBER: US/09/742,693
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: EP99310431.4
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5

LENGTH: 36

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Primer

US-09-742-693-5

Query Match 57.1%; Score 16; DB 4; Length 36;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGAACTGCATCCAAATTCAGGTTTC 28
|||||
DB 13 GGAGCTGCATGCAAAATTCATTTC 36

RESULT 8
PCT-US95-11405-20
; Sequence 20, Application PC/TUS9511405
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PHOSPHOROUS-32 LABELING OF ANTIBODIES
; TITLE OF INVENTION: FOR CANCER THERAPY
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11405
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,103
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/599/IWIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-11405-20

Query Match 54.3%; Score 15.2; DB 5; Length 40;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GTCTGGAAGTGCATCCAAATTCAGGTTTC 28
Db 11 GCCGAGATCTGCATGCAAAATTCATTTC 38

RESULT 9
US-07-938-084-15
; Sequence 15, Application US/07938084
; Patent No. 5464945
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Rebecca L.
; APPLICANT: Walsh, P. Sean
; TITLE OF INVENTION: A Chemiluminescent Method for the
; TITLE OF INVENTION: Quantitation of Human DNA
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/938,084
; FILING DATE: 19920828
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8669
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 522-1285
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-938-084-15

Query Match 53.6%; Score 15; DB 1; Length 43;
Best Local Similarity 78.3%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GAATGTCATCCAAATTCAGGTTTC 28
Db 1 GAACGTATCGACATCTGGTTTC 23

RESULT 10
US-08-459-135A-3
; Sequence 3, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPEA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 base pairs
; TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: GENOMIC DNA
US-08-459-135A-3

Query Match          53.6%; Score 15; DB 2; Length 68;
Best Local Similarity 78.3%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAAGTGCATCCAAATTCAG 24
Db 46 TCTGGATCCGCATCGCAATTCGG 68

RESULT 11
US-08-459-135A-4
; Sequence 4, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: GENOMIC DNA
US-08-459-135A-4

Query Match          53.6%; Score 15; DB 2; Length 68;
Best Local Similarity 78.3%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAAGTGCATCCAAATTCAG 24
Db 46 TCTGGATCCGCATCGCAATTCGG 68

RESULT 12
US-08-459-559-3

; Sequence 3, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURNAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-08-495-559-3

Query Match          53.6%; Score 15; DB 3; Length 68;
Best Local Similarity 78.3%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAAGTGCATCCAAATTCAG 24
Db 46 TCTGGATCCGCATCGCAATTCGG 68

RESULT 13
US-08-495-559-4
; Sequence 4, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURNAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-08-495-559-4

Query Match          53.6%; Score 15; DB 3; Length 68;
Best Local Similarity 78.3%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAAGTGCATCCAAATTCAG 24
Db 46 TCTGGATCCGCATCGCAATTCGG 68

RESULT 14
US-09-140-466-9/c
; Sequence 9, Application US/09140466
; Patent No. 6268160
; GENERAL INFORMATION:
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; APPLICANT: CLOUGH, BARBARA
; APPLICANT: PREISER, PETER
; APPLICANT: WILSON, ROBERT
; TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
; TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
; TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
; FILE REFERENCE: N68837B GCM PJC DP
; CURRENT APPLICATION NUMBER: US/09/140,466
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/056,246
; EARLIER FILING DATE: 1997-08-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 58
; TYPE: RNA
; ORGANISM: Plasmodium falciparum
US-09-140-466-9

Query Match 52.1%; Score 14.6; DB 3; Length 58;
Best Local Similarity 81.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 AACTGCATCCAAATTCAGTT 27
|||||
DB 26 AACTGCTTCCAAATTTACTTT 6

RESULT 15
US-09-140-466-10/c
; Sequence 10, Application US/09140466
; Patent No. 6268160
; GENERAL INFORMATION:
; APPLICANT: CLOUGH, BARBARA
; APPLICANT: PREISER, PETER
; APPLICANT: WILSON, ROBERT
; TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
; TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
; TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
; FILE REFERENCE: N68837B GCM PJC DP
; CURRENT APPLICATION NUMBER: US/09/140,466
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/056,246
; EARLIER FILING DATE: 1997-08-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 58
; TYPE: RNA
; ORGANISM: Plasmodium falciparum
US-09-140-466-10

Query Match 52.1%; Score 14.6; DB 3; Length 58;
Best Local Similarity 81.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 AACTGCATCCAAATTCAGTT 27
|||||
DB 26 AACTGCTTCCAAATTTACTTT 6

Search completed: September 1, 2004, 23:07:49
Job time : 50 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 22:39:33 : Search time 242 Seconds
(without alignments)
569.421 Million cell updates/sec

Title: US-10-028-415-2
Perfect score: 28
Sequence: 1 gcttggactgcattccaaattcaggttc 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 323270 seqs, 2460713050 residues
Total number of hits satisfying chosen parameters: 2018620

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA:*
- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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 - 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 - 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
 - 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 - 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 - 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 - 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 - 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	28	100.0	28	10	US-09-997-905A-29
c 2	28	100.0	28	14	US-10-028-415-2
c 3	28	100.0	28	14	US-10-028-415-11
c 4	17.2	61.4	65	10	US-09-908-975-28733
c 5	16.6	59.3	60	10	US-09-908-975-9817
c 6	16	57.1	36	9	US-09-742-693-5
c 7	16	57.1	36	15	US-10-112-261B-10
c 8	15.8	56.4	50	16	US-10-131-827-4796
c 9	15.6	55.7	60	10	US-09-908-975-12681
c 10	15.6	55.7	60	10	US-09-908-975-1746
c 11	15.4	55.0	65	10	US-09-908-975-7331
c 12	15.2	54.3	65	15	US-10-032-585-3449
c 13	15.2	54.3	65	15	US-10-032-750-212
c 14	15	53.6	24	13	US-10-308-264-697

c 15 14.8 52.9 27 10 US-09-997-905A-12
c 16 14.8 52.9 60 10 US-09-908-975-18855
c 17 14.8 52.9 60 10 US-09-908-975-19479
c 18 14.8 52.9 60 10 US-09-908-975-20568
c 19 14.6 52.1 41 12 US-10-035-833A-3049
c 20 14.6 52.1 41 12 US-10-035-833A-5559
c 21 14.6 52.1 58 9 US-09-845-335-9
c 22 14.6 52.1 58 9 US-09-845-335-10
c 23 14.6 52.1 65 15 US-10-032-585-2841
c 24 14.6 52.1 30 15 US-10-092-263-5
c 25 14.4 51.4 47 16 US-10-349-143-3861
c 26 14.4 51.4 59 8 US-08-781-986A-5133
c 27 14.4 51.4 59 13 US-10-329-624-5133
c 28 14.4 51.4 60 10 US-09-908-975-6927
c 29 14.4 51.4 60 10 US-09-908-975-18337
c 30 14.4 51.4 60 10 US-09-908-975-32090
c 31 14.4 51.4 60 10 US-09-908-975-32302
c 32 14.4 51.4 60 16 US-10-269-695-187
c 33 14.4 51.4 60 16 US-10-410-998-187
c 34 14.2 50.7 22 15 US-10-005-338B-184
c 35 14.2 50.7 39 9 US-09-925-664-35
c 36 14.2 50.7 39 12 US-09-925-182-35
c 37 14.2 50.7 54 13 US-09-837-306-187
c 38 14.2 50.7 54 16 US-10-045-674-490
c 39 14.2 50.7 60 10 US-09-908-975-18477
c 40 14.2 50.7 60 10 US-09-908-975-23008
c 41 14.2 50.7 65 10 US-09-908-975-29773
c 42 14.2 50.7 88 9 US-09-864-761-23913
c 43 14 50.0 14 14 US-10-028-415-9
c 44 14 50.0 14 14 US-10-028-415-10
c 45 14 50.0 14 14 US-10-028-415-12

ALIGNMENTS

RESULT 1
US-09-997-905A-29/c
; Sequence 29, Application US/09997905A
; Publication No. US20030074684A1
; GENERAL INFORMATION:
; APPLICANT: Benitec Australia Ltd
; APPLICANT: State of Queensland through its Department of Primary Industries
; TITLE OF INVENTION: Control of Gene Expression
; FILE REFERENCE: M80219470
; CURRENT APPLICATION NUMBER: US/09/997,905A
; CURRENT FILING DATE: 2002-11-30
; PRIOR APPLICATION NUMBER: US 09/100,812
; PRIOR FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 28
; TYPE: DNA
; ORGANISM: double-stranded
US-09-997-905A-29

Query Match 100.0%; Score 28; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGGAACTGCATCCAAATTCAGGTTC 28
Db 28 GCTTGGAACTGCATCCAAATTCAGGTTC 1

RESULT 2
US-10-028-415-2
; Sequence 2, Application US/10028415
; Publication No. US20020151063A1
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; APPLICANT: Watson, James D.

```

; TITLE OF INVENTION: Methods for Modulating Apoptotic Cell
; TITLE OF INVENTION: Death
; FILE REFERENCE: 11000.1004c3
; CURRENT APPLICATION NUMBER: US/10/028,415
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/NZ01/00286
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 09/724,809
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/036,004
; PRIOR FILING DATE: 1998-03-04
; PRIOR APPLICATION NUMBER: US 08/713,557
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Human
US-10-028-415-2

```

```

Query Match 100.0%; Score 28; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
DB 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28

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RESULT 3

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US-10-028-415-11/c
; Sequence 11, Application US/10028415
; Publication No. US20020151063A1
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Methods for Modulating Apoptotic Cell
; TITLE OF INVENTION: Death
; FILE REFERENCE: 11000.1004c3
; CURRENT APPLICATION NUMBER: US/10/028,415
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/NZ01/00286
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 09/724,809
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/036,004
; PRIOR FILING DATE: 1998-03-04
; PRIOR APPLICATION NUMBER: US 08/713,557
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Human
US-10-028-415-11

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Query Match 100.0%; Score 28; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
DB 28 GTCGGAAGTGCATCCAAATTCAGGTTTC 1

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RESULT 4

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US-09-908-975-28733/c
; Sequence 28733, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi

```

```

; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28733
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-28733

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Query Match 61.4%; Score 17.2; DB 10; Length 65;
Best Local Similarity 86.4%; Pred. No. 4.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 3 CTGGAAGTGCATCCAAATTCAG 24
DB 61 CTGCACTGCGAGCCAAATTCAG 40

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RESULT 5

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US-09-908-975-9817/c
; Sequence 9817, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9817
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-9817

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Query Match 59.3%; Score 16.6; DB 10; Length 60;
Best Local Similarity 82.6%; Pred. No. 8.5e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 3 CTGGAAGTGCATCCAAATTCAGG 25
DB 35 CTGTCCTGCGTCCAAAGTCAGG 13

```

RESULT 6

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US-09-742-693-5
; Sequence 5, Application US/09742693
; Patent No. US20020019324A1
; GENERAL INFORMATION:
; APPLICANT: HOWELL, Steven
; APPLICANT: LITTLE, Julie C.

```

```

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4796
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-4796

Query Match      56.4%; Score 15.8; DB 16; Length 50;
Best Local Similarity 74.1%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      2  CTCGGACTGCATCCCAATTTCAGGTTTC 28
      ||||| ||| ||||| ||||| |||||
DB      24  TCTGGTACTAGTACAAAATTCGGTTTC 50

RESULT 9
US-09-908-975-12681/c
; Sequence 12681, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12681
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-908-975-12681

Query Match      55.7%; Score 15.6; DB 10; Length 60;
Best Local Similarity 81.8%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3  CTGGAAGTGCATCCCAATTTCAG 24
      ||||| ||| ||||| |||||
DB      46  CAGGAAGTGCACCCAGATTCCG 25

RESULT 10
US-09-908-975-1746
; Sequence 1746, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING

```

/ TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
/ FILE REFERENCE: 36688-0005
/ CURRENT APPLICATION NUMBER: US/09/908,975
/ CURRENT FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/287,724
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/221,607
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 32337
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1746
/ LENGTH: 65
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-09-908-975-1746

Query Match 55.7%; Score 15.6; DB 10; Length 65;
Best Local Similarity 81.8%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTGGAAGTGCATCCAAATTC 22
| | | | | | | | | | | | | | | | | | | | | |
DB 23 GGCTGGAAGTGAAGCCAAATTC 44

RESULT 11
US-09-908-975-7331/c
/ Sequence 7331, Application US/09908975
/ Publication No. US20030165843A1
/ GENERAL INFORMATION:
/ APPLICANT: SHOSHAN, Avi
/ APPLICANT: WASSERMAN, Alon
/ APPLICANT: MINTZ, Eli
/ APPLICANT: MINTZ, Liat
/ APPLICANT: FAIGLER, Simchon
/ TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
/ FILE REFERENCE: 36688-0005
/ CURRENT APPLICATION NUMBER: US/09/908,975
/ CURRENT FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/287,724
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/221,607
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 32337
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 7331
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-908-975-7331

Query Match 55.0%; Score 15.4; DB 10; Length 60;
Best Local Similarity 76.0%; Pred. No. 3.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 CTGGAAGTGCATCCAAATTCAGGTT 27
| | | | | | | | | | | | | | | | | | | | | |
DB 47 CTGGGACTGCAACCAACTCAGGTT 23

RESULT 12
US-10-032-585-3449
/ Sequence 3449, Application US/10032585
/ Publication No. US20030180953A1
/ GENERAL INFORMATION:
/ APPLICANT: Terry Roemer D.
/ APPLICANT: Bo, Jiang
/ APPLICANT: Charles, Boone
/ APPLICANT: Howard, Bussey
/ TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
/ FILE REFERENCE: 10182-005-999
/ CURRENT APPLICATION NUMBER: US/10/032,585

/ CURRENT FILING DATE: 2001-12-20
/ NUMBER OF SEQ ID NOS: 8000
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3449
/ LENGTH: 65
/ TYPE: DNA
/ ORGANISM: Cardida albicans
US-10-032-585-3449

Query Match 54.3%; Score 15.2; DB 15; Length 65;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGGAACTGCATCCAAATTC 23
| | | | | | | | | | | | | | | | | | | | | |
DB 18 TGGACCAGCATCCAAATCA 37

RESULT 13
US-10-092-750-212
/ Sequence 212, Application US/10092750
/ Publication No. US20030032157A1
/ GENERAL INFORMATION:
/ APPLICANT: Hammond, Philip W.
/ APPLICANT: Alpin, Julia
/ APPLICANT: Wright, Martin C.
/ TITLE OF INVENTION: Polypeptides Interactive with BCL-XL
/ FILE REFERENCE: 50036/050002
/ CURRENT APPLICATION NUMBER: US/10/092,750
/ CURRENT FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 60/274,526
/ PRIOR FILING DATE: 2001-03-08
/ NUMBER OF SEQ ID NOS: 253
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 212
/ LENGTH: 84
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 147
/ OTHER INFORMATION: n = A,T,C or G
US-10-092-750-212

Query Match 54.3%; Score 15.2; DB 15; Length 84;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGGAACTGCATCCAAATTC 23
| | | | | | | | | | | | | | | | | | | | | |
DB 34 TGGAACTGCATCCAAACTTA 53

RESULT 14
US-10-308-264-697/c
/ Sequence 697, Application US/10308264
/ Publication No. US20040029133A1
/ GENERAL INFORMATION:
/ APPLICANT: Herrnstadt, Corinna
/ TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
/ FILE REFERENCE: 660088.461
/ CURRENT APPLICATION NUMBER: US/10/308,264
/ CURRENT FILING DATE: 2002-11-25
/ NUMBER OF SEQ ID NOS: 697
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 697
/ LENGTH: 24
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
US-10-308-264-697

Query Match 53.6%; Score 15; DB 13; Length 24;
Best Local Similarity 78.3%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 GAATGCTCCCAATTCAGGTTT 28
Db 24 GAATGCTCCGACATCTGTTT 2

RESULT 15
US-09-997-905A-12/c
; Sequence 12, Application US/09997905A
; Publication No. US20030074684A1
; GENERAL INFORMATION:
; APPLICANT: Benitec Australia Ltd
; TITLE OF INVENTION: State of Queensland through its Department of Primary Industries
; FILE REFERENCE: M80219470
; CURRENT APPLICATION NUMBER: US/09/997,905A
; CURRENT FILING DATE: 2002-11-30
; PRIOR APPLICATION NUMBER: US 09/100,812
; PRIOR FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 27
; TYPE: DNA
; ORGANISM: virus
US-09-997-905A-12

Query Match 52.9%; Score 14.8; DB 10; Length 27;
Best Local Similarity 73.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCTGGAACCTGCATCCCAATTCAGGTT 27
Db 26 TCTGGAACCTGGTAGAAGTTAACGTT 1

Search completed: September 1, 2004, 23:42:42
Job time : 244 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 22:35:18 ; Search time 1765 Seconds
(without alignments)
473.734 Million cell updates/sec

Title: US-10-028-415-2

Perfect score: 28

Sequence: 1 gcttgaactgcatccaaattcaggttc 28

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 569298

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_esttc.*
9: gb_estti.*
10: gb_estc2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_lam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	18.4	65.7	67	14	CD881233
2	16.6	59.3	85	9	AU265805
3	16	57.1	52	10	AW396361
4	16	57.1	64	10	BE638254

C 5	15.8	56.4	73	13	BQ086192
C 6	15.8	56.4	73	29	CG532825
C 7	15.8	56.4	91	9	AA814152
C 8	15.8	56.4	100	28	AZ761676
C 9	15.6	55.7	66	14	CD946266
C 10	15.6	55.7	67	14	CD946207
C 11	15.2	54.3	50	9	AU105882
C 12	15.2	54.3	56	10	AW268320
C 13	15.2	54.3	59	12	BJ041364
C 14	15.2	54.3	61	9	AI174615
C 15	15.2	54.3	76	9	AA671040
C 16	15.2	54.3	88	9	AI000664
C 17	15.2	54.3	89	12	BI490973
C 18	15.2	54.3	95	9	AI855768
C 19	15.2	54.3	98	10	BE138707
C 20	15	53.6	50	9	AU102350
C 21	15	53.6	50	9	AU102351
C 22	15	53.6	50	9	AU105884
C 23	15	53.6	84	29	CG564129
C 24	15	53.6	92	14	CA803412
C 25	15	53.6	94	29	CG646872
C 26	14.8	52.9	45	28	BH850369
C 27	14.8	52.9	58	9	AL805765
C 28	14.8	52.9	60	14	D45451
C 29	14.8	52.9	61	28	BH863711
C 30	14.8	52.9	77	9	AA980728
C 31	14.8	52.9	82	29	CNS041CQ
C 32	14.8	52.9	85	12	BI407547
C 33	14.8	52.9	94	14	N40508
C 34	14.8	52.9	98	28	CC019463
C 35	14.6	52.1	59	10	BG041906
C 36	14.6	52.1	95	14	CB187735
C 37	14.4	51.4	67	9	AA654686
C 38	14.4	51.4	79	13	B0637417
C 39	14.4	51.4	87	14	Z20306
C 40	14.4	51.4	100	14	T97877
C 41	14.2	50.7	43	28	AZ803705
C 42	14.2	50.7	50	9	AU104942
C 43	14.2	50.7	54	13	BX551631
C 44	14.2	50.7	58	9	AL659070
C 45	14.2	50.7	61	29	CNS02YTI

ALIGNMENTS

RESULT 1
CD881233
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD881233 67 bp mRNA linear EST 14-JUL-2003
F1.102G08F010328 F1 Triticum aestivum cDNA clone F1102G08, mRNA
sequence.

CD881233.1 GI:32640120

EST.

Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Triticum.

1 (bases 1 to 67)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>)

and <http://genoplante-info.infobiogen.fr>.

Location/Qualifiers

1..67

FEATURES

source

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/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="F102G08"
/tissue_type="leaf one"
/clone_lib="F1"

ORIGIN
Query Match      65.7%; Score 18.4; DB 14; Length 67;
Best Local Similarity 78.6%; Pred. No. 2e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GTCGGAACTGCATCCAAATTCAGGTTTC 28
    |||||
Db 32 GTCGGAACTGAAACTAAATTAAGGTGC 59

RESULT 2
AU265805      85 bp mRNA linear EST 10-MAY-2002
LOCUS AU265805 VS Dictyostelium discoideum cDNA clone VSP794 3', mRNA
DEFINITION AU265805 VS Dictyostelium discoideum cDNA clone VSP794 3', mRNA
ACCESSION AU265805
VERSION AU265805
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 85)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriiki,E., Ochiai,H., Maeda,M.,
        Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular
        stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
        Institute of Biological Sciences
        University of Tsukuba
        1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
        Tel: 81-298-53-4664
        Fax: 81-298-53-6614
        Email: hideko@biol.tsukuba.ac.jp.
        Location/Qualifiers
FEATURES             source
     1..85
     /organism="Dictyostelium discoideum"
     /mol_type="mRNA"
     /strain="AX4"
     /db_xref="taxon:44689"
     /clone="VSP794"
     /sex="mat A"
     /dev_stage="vegetative"
     /clone_lib="VS"

ORIGIN
Query Match      59.3%; Score 16.6; DB 9; Length 85;
Best Local Similarity 79.2%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGAAGTGCATCCAAATTCAGGTTTC 28
    |||||
Db 39 GGAGTTCGTTACAAATTCAGGTTTC 62

RESULT 3
AW396361/c     52 bp mRNA linear EST 03-DEC-2001
LOCUS AW396361 sh27b06.y1 Gm-cl016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl016-5964 5', mRNA sequence.
ACCESSION AW396361
VERSION AW396361
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

/organism="Glycine max"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="F102G08"
/tissue_type="leaf one"
/clone_lib="F1"

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 52)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Varra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean Est Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Hunttsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 252 Std Error: 0.00
Seq primer: -40RP from Gibco.
Location/Qualifiers
     1..52
     /organism="Glycine max"
     /mol_type="mRNA"
     /db_xref="taxon:3847"
     /clone="GENOME SYSTEMS CLONE ID: Gm-cl016-5964"
     /tissue_type="immature flowers of field grown plants"
     /lab_host="XL10-Gold"
     /clone_lib="Gm-cl016"
     /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dt) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelding."

ORIGIN
Query Match      57.1%; Score 16; DB 10; Length 52;
Best Local Similarity 79.2%; Pred. No. 1.8e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTGGAACTGCATCCAAATTCAGGT 26
    |||||
Db 50 CTCTAACTGAATCCCAATTCAGTT 27

RESULT 4
BE638254      64 bp mRNA linear EST 28-AUG-2000
LOCUS BE638254 SMOVMFCAR17A08SK Onchocerca volvulus microfilaria cDNA
DEFINITION (SAW98MLW-Ovmf) Onchocerca volvulus cDNA clone SMOVMFCAR17A08 5',
        mRNA sequence.
ACCESSION BE638254
VERSION BE638254.1 GI:9931997
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
1 (bases 1 to 64)

```


AUTHORS **TITLE** **JOURNAL** **COMMENT**

Williams, S.A.
Genes expressed in microfilaria of Onchocerca volvulus
Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers

FEATURES

source
1..64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SMOVMFCAR17A08"
/dev_stage="microfilaria"
/lab_host="X11-Blue MRP"
/clone_lib="Onchocerca volvulus microfilaria cDNA
(SAW98LW-OvMF)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. mRNA was
prepared from approximately 200,000 microfilariae isolated
from the skin of infected individuals from Kumba,
Cameroon and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library has 7.8 x 10E4 independent
recombinants and the average insert size is approximately
1kb. The library was constructed by Michelle
Lizotte-Waniewski. The library is available from
Dr. S.A. Williams, email: genome@smith.edu."

ORIGIN

Query Match 57.18; Score 16; DB 10; Length 64;
Best Local Similarity 79.21; Pred. No. 2e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAAGTGCATCCAAATTCAGGTTTC 28
|||||
Db 8 GGAAGTGCATCCAAATTCAGGTTTC 31

RESULT 5

BQ086192/c
LOCUS BQ086192 73 bp mRNA linear EST 29-APR-2002
DEFINITION i19f02.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6135291 5', mRNA sequence.

ACCESSION BQ086192.1 GI:20045396
VERSION BQ086192.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 73)

REFERENCE 1
AUTHORS Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hallier, I., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

TITLE

Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

JOURNAL

Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LBNL; please contact the IMAGE
consortium (info@image.lbl.gov) for further information
Putative full length read
vector to vector length is 74
Seq primer: -40RP from Gibco.

FEATURES source

1..73
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6135291"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPOR1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

ORIGIN

Query Match 56.44; Score 15.8; DB 13; Length 73;
Best Local Similarity 74.11; Pred. No. 2.5e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TCTGGAATGCATCCAAATTCAGGTTTC 28
|||||
Db 30 TCGGGAAGTAAACCCAAAGGCAGGCTC 4

RESULT 6

CG532825/c
LOCUS CG532825 73 bp DNA linear GSS 01-OCT-2003

DEFINITION OST117228 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST117228, genomic survey sequence.

ACCESSION CG532825
VERSION CG532825.1 GI:37319397

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 73)

REFERENCE 1
AUTHORS Zambronic, B.P., Abuin, A., Ramirez-Solis, R., Richer, L.J.,
Pigott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):1608-11)

```

FEATURES
  source
    Class: Gene Trap.
    Location/Qualifiers
      1..73
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="129SV/EV"
        /db_xref="taxon:10090"
        /clone="OST117228"
        /cell_type="embryonic stem cell"
        /clone_lib="Mus musculus 129SV/Ev"

ORIGIN
  Query Match      55.4%; Score 15.8; DB 29; Length 73;
  Best Local Similarity 71.4%; Pred. No. 2.5e+04;
  Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GTCGGAACTGCATCCAAATTCAGGTTTC 28
Db 60 GTAATGNACTGCATGCACACTCAAGTTC 33

RESULT 7
LOCUS      AA814152      91 bp      mRNA      linear      EST 05-MAR-1998
DEFINITION 0025e02.51 NCI_CGAP Kids Homo sapiens cDNA clone IMAGE1324730 3',
            mRNA sequence.
ACCESSION  AA814152
VERSION     AA814152.1 GI:2883748
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 91)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-rc@mail.nih.gov
            unknown library type
            Insert Length: 1415 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 77.

FEATURES
  source
    1..91
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:1324730"
      /tissue_type="2 pooled tumors (clear cell type)"
      /lab_hosts="DH10B"
      /clone_lib="NCI CGAP Kids"
      /note="Organ: kidney; Vector: pTTT3D-Pac (Pharmacia) with
            a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5',
            AACTGGAAGAAATTCGGCGCGCAATATTTTCTTTTCTTTT 3'],
            double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I
            and Eco RI sites of the modified pTTT3 vector. Library
            went through one round of normalization. Library
            constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
  Query Match      56.4%; Score 15.8; DB 9; Length 91;
  Best Local Similarity 74.1%; Pred. No. 2.6e+04;
  Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TCTGGAATGCATCCAAATTCAGGTTTC 28
Db 69 TCTGGTACTAGCTACAAATTCGGTTTC 43

FEATURES
  source
    100 bp      DNA      linear      GSS 16-FEB-2001
    1M0556D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
    clone UUGC1M0556D07 F, genomic survey sequence.
    A2761676
    A2761676
    A2761676.1 GI:12870848
    GSS.
    Mus musculus (house mouse)
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 100)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.,
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0556 row: D column: 07
    Seq primer: CGTTGTAACGACGCGCCAGT
    Class: plasmid ends
    High quality sequence stop: 100.
    Location/Qualifiers
      1..100
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0556D07"
        /sex="Male"
        /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: pWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adapted DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adapted mouse DNA was annealed to
            adapted vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

ORIGIN
  Query Match      55.4%; Score 15.8; DB 28; Length 100;
  Best Local Similarity 74.1%; Pred. No. 2.7e+04;
  Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TCTGGAATGCATCCAAATTCAGGTTTC 28
Db 25 TATGGAAATGCATCCAAATTCAGTTC 51

```

```

ORIGIN

Query Match      55.7%; Score 15.6; DB 14; Length 67;
Best Local Similarity 81.8%; Pred. NO. 2.9e+04;
Matches: 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 CTGGAAGCTGCATCCCAATTCCAG 24
      | | | | | | | | | | | | | |
DB      30 CAGAAACCGCATCCACATTCCAG 51

RESULT 11
LOCUS   AU105882
DEFINITION AU105882 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION KAT058774, mRNA sequence.
VERSION   AU105882
KEYWORDS  AU105882.1 GI:13555403
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Sasaki, Y., Taifu, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
          Hata, H., Oca, T., Isozaki, T., Tanaka, T., Morishita, S., Okubo, K.,
          Sasaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE  21270072

```

11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshimoto-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

```

FEATURES
    source
        1. 50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="KAT08774"
            /clone_lib="Sugano Homo sapiens cDNA library"
            Location/Qualifiers
                origin
                    Query Match          54.3%;   Score 15.2;   DB 9;   Length 50;
                    Best Local Similarity 71.4%;   Pred. No. 3.9e+04;
                    Matches 20;   Conservative 0;   Mismatches 8;   Indels 0;   Gaps 0;

Qy      1  GTCTGGAACTGCATCCAAATTCAGGTTTC 28
          |||||
Db      5  GCCTGCATCTGTATCCAGTGTCAGGTCC 32

```

RESULT 12
 LOCUS AW268320 56 bp mRNA linear EST 03-JAN-2000
 DEFINITION x195f11.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767917 3',
 mRNA sequence.
 ACCESSION AW268320
 VERSION AW268320
 KEYWORDS GI:6655350
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 56)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rcmail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/borp/image/image.html

Possible reversed clone: polyT not found

Seq primer: -40UP from Gibco.

FEATURES
source

1..56
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2767917"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu26"
/note="Organ: lung; Vector: pAMP1; mRNA made from lung
adenocarcinoma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

ORIGIN

Query Match 54.3%; Score 15.2; DB 10; Length 56;
Best Local Similarity 71.4%; Pred. No. 4.1e+04;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GTCGGAAGTCATCCCAAAATTCAGGTC 28
||||| ||| ||||| |||||
DB 25 GTCGCCCCCTCATTAATAAATTCAGGTC 52

RESULT 13

BJ041364/c
LOCUS BJ041364 59 bp mRNA linear EST 29-SEP-2003
DEFINITION BJ041364 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL008e05 5', mRNA sequence.

ACCESSION BJ041364

VERSION BJ041364.1 GI:17412190

KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 59)

AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and

Kohara,Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

CONTACT Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp

The information of this clone is available through the following

URL.

http://xenopus.nibb.ac.jp.

Location/Qualifiers

FEATURES

source
1..59
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"

ORIGIN
/clone="XL008e05"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"

Query Match 54.3%; Score 15.2; DB 12; Length 59;
Best Local Similarity 85.0%; Pred. No. 4.1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCTGGAAGTCATCCCAAAAT 21
||||| ||||| |||||

DB 23 TCTGATCTGCATCCAAAT 4
||||| ||||| |||||

RESULT 14

AI174615

LOCUS

DEFINITION

AI174615

61 bp mRNA linear EST 07-OCT-1998

an47d11.s1 Gessler Wilms tumor Homo sapiens cDNA clone

IMAGE:1701813 3', similar to SW:ATP6_TRYBB P24499 ATP SYNTHASE A

CHAIN; mRNA sequence.

ACCESSION AI174615

VERSION AI174615.1 GI:3721468

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 61)

AUTHORS

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project

Unpublished (1997)

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..61

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1701813"

/sex="pooled (6)"

/lab_host="DH10B"

/clone_lib="Gessler Wilms tumor"

/note="Vector: pSPOR1; Site: 1; SalI; Site 2: NotI; RNA

was prepared from a pool of 6 anonymous Wilms' tumor RNAs.

RNA was prepared by acid-phenol, followed by one round of

oligo dT selection. cDNA library preparation was with

the BRL/Life Tech. Superscript Plasmid system. An

oligo-dT NotI primer for first strand synthesis generated

9cggccgccc(t)n at the 3' end of the clones. A 5' SalI

adaptor was used with sequence 5'-gtcgaccacgctcg-3'.

Resulting cDNAs were size selected (average size 2 Kb),

NotI digested, and ligated into NotI/SalI-cut pSPORT1.

Library was constructed by Dr. Manfred Gessler."

ORIGIN

Query Match 54.3%; Score 15.2; DB 9; Length 61;

Best Local Similarity 85.0%; Pred. No. 4.1e+04;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AACTGCATCCAAATTCAGGT 26
|||||
Db 17 AACTGAATCCCAAGTCAGGT 36

RESULT 15
AA671040/c
LOCUS
DEFINITION
AA671040 76 bp mRNA linear EST 25-NOV-1997
vis1f01.r1 Beddington mouse embryonic region Mus musculus cDNA
clone IMAGE:907321 5' similar to TR:G192989 G192989 ELONGATION
FACTOR 2 ; mRNA sequence.
AA671040
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 76)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theisinger,B., Wylie,F., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE
JOURNAL
COMMENT
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marta M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG:527985
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..76
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6 x DBA"
/db_xref="taxon:10090"
/clone="IMAGE:907321"
/sex="pooled"
/tissue_type="embryo"
/dev_stages="7.5dpc"
/lab_host="DH12S"
/clone_lib="Beddington mouse embryonic region"
/note="Organ: whole embryo; Vector: pCMV-SPORT; Site 1:
Salt; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Gastrulating embryos were collected at 7.5dpc
from C57BL/6 x DBA matings, excluding embryos that had
developed head folds and all extraembryonic tissues.
Average insert size: 1.3 kb (range: 0.5 - 3.0 Kb).
Referenced in Development 121, 2479-2489 (1995)"

ORIGIN
Query Match 54.3%; Score 15.2; DB 9; Length 76;
Best Local Similarity 85.0%; Pred.No.4.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 GAATGCATCCAAATTCAGG 25
|||||
Db 32 GAACCGCATCAAAATGCAGG 13

Search completed: September 1, 2004, 23:38:32
Job time : 1769 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 17:24:51 ; Search time 233 Seconds
(without alignments)
510.513 Million cell updates/sec

Title: US-10-028-415-2
Perfect score: 28
Sequence: 1 gctggaactgcattccaaattcagggttc 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	2 AAV20897	AAV20897 CD95 regu
C 2	28	100.0	28	2 AAV23143	AAV23143 CD95 regu
C 3	28	100.0	28	6 ABK88709	ABK88709 Human CD9
4	28	100.0	28	6 ABK88700	ABK88700 Transcrip
5	28	100.0	50	2 AAV23172	AAV23172 CD95 enha
6	28	100.0	1608	2 AAT34162	AAT34162 Fas promo
7	28	100.0	2165	6 ABN79677	ABN79677 Sequence
8	28	100.0	28118	9 ADE43798	ADE43798 Polymorph
9	28	100.0	28118	9 ADE43797	ADE43797 Human TNF
10	28	100.0	45121	8 ADA02744	ADA02744 Human TNF
11	28	100.0	45121	9 ADB72482	ADB72482 Human TNF
12	28	100.0	45121	9 ADC85224	ADC85224 Human Tnf
C 13	20	71.4	9193	6 AAD46346	AAV23143 CD95 regu
C 14	19	67.9	1608	6 ABL34419	ABL34419 Human imm
C 15	19	67.9	108359	8 ADA13316	ADA13316 Human fri
C 16	19	67.9	160771	6 ABQ88179	ABQ88179 Human ost
C 17	18.8	67.1	1424	6 ABZ33746	ABZ33746 Human TRI
C 18	18.6	66.4	460	6 ABN21606	ABN21606 Human ORF
C 19	18.6	66.4	508	8 ACH36880	ACH36880 Human end
C 20	18.6	66.4	525	4 AAH09866	AAH09866 Human CDN
C 21	18.6	66.4	1487	4 AAH13934	AAH13934 Human CDN
C 22	18.6	66.4	2287	5 ABA14736	ABA14736 Human ner
C 23	18.6	66.4	2287	5 ABA14735	ABA14735 Human ner

C 24	18.6	66.4	3191	3 AAZ58978	AAZ58978 Human cyt
C 25	18.6	66.4	3363	5 AAS45004	AAS45004 CDNA enco
C 26	18.4	65.7	501	8 ACH35087	ACH35087 Human end
C 27	18.4	65.7	509	2 AAZ34186	AAZ34186 Human EST
C 28	18.4	65.7	509	3 AAC78546	AAC78546 Human EST
C 29	18.4	65.7	509	5 AAF93396	AAF93396 Aortic en
C 30	18.4	65.7	509	7 ACD42719	ACD42719 Novel hum
C 31	18.4	65.7	509	7 ACA63754	ACA63754 Novel hum
C 32	18.4	65.7	509	7 ACA71918	ACA71918 Human PRO
C 33	18.4	65.7	509	7 ABX92558	ABX92558 Human PRO
C 34	18.4	65.7	509	7 ACA66299	ACA66299 Human sec
C 35	18.4	65.7	509	8 ADA24886	ADA24886 Novel hum
C 36	18.4	65.7	509	8 ACD29900	ACD29900 Novel hum
C 37	18.4	65.7	509	8 ADA12547	ADA12547 Human sec
C 38	18.4	65.7	509	8 ACD29315	ACD29315 Novel hum
C 39	18.4	65.7	509	9 ADB73853	ADB73853 Human PRO
C 40	18.4	65.7	509	9 ADB78569	ADB78569 Human PRO
C 41	18.4	65.7	509	9 ADC43995	ADC43995 Human EST
C 42	18.4	65.7	509	9 ADC61755	ADC61755 Human EST
C 43	18.4	65.7	509	9 ADC63719	ADC63719 Human EST
C 44	18.4	65.7	509	9 ADC66819	ADC66819 Human EST
C 45	18.4	65.7	509	9 ADC68943	ADC68943 Human EST

ALIGNMENTS

RESULT 1
AAV20897
ID AAV20897 standard; DNA; 28 BP.

XX AC AAV20897;

XX XX 23-JUL-1998 (first entry)

XX DE CD95 regulatory region.

XX XX CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;

KW cancer; viral infection; neurodegeneration; autoimmune disease;

KW gene therapy; transcription factor; ss.

XX OS Homo sapiens.

XX XX WO9808965-A2.

XX XX 05-MAR-1998.

XX XX 29-AUG-1997; 97WO-NZ000107.

XX XX 30-AUG-1996; 96US-00713557.

XX XX (GENE-) GENESIS RES & DEV CORP LTD.

XX XX Watson JD, Rudert F;

XX XX WPI; 1998-179445/16.

XX New regulatory regions from the CD95 gene and transcription factors that interact with them - for control of apoptosis, e.g. in treatment of cancer, viral infection, neurodegeneration and autoimmune disease.

XX Claim 1; Page 36; 60pp; English.

XX This sequence represents a regulatory region from the CD95 gene, and is a nucleic acid of the invention. The regulatory regions (silencers or enhancers) are involved in apoptosis, i.e. inhibition of CD95 expression will inhibit apoptosis. Regulation of apoptosis is useful in treatment of cancer, (retroviral infection, neurodegeneration and autoimmune disease, e.g. by gene therapy for expressing transcription factors or expression of antisense sequences to inhibit transcription factor production. The regulatory nucleic acids and transcription factors are also useful for studying regulation of CD95 in vitro or in vivo, to screen for modulators and as probes to isolate related genes

```

XX SQ Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28
Db 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28

RESULT 2
AAV23143/c
ID AAV23143 standard; DNA; 28 BP.
XX AC AAV23143;
XX AC AAV23143;
XX DT 23-JUL-1998 (first entry)
XX DE CD95 regulatory region.
XX KW CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;
XX KW cancer; viral infection; neurodegeneration; autoimmune disease;
XX KW gene therapy; transcription factor; ss.
XX OS Homo sapiens.
XX FN WO9808965-A2.
XX PD 05-MAR-1998.
XX PF 29-AUG-1997; 97WO-NZ000107.
XX PR 30-AUG-1996; 96US-00713557.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Watson JD, Rudert F;
XX DR WPI; 1998-179445/16.
XX PT New regulatory regions from the CD95 gene and transcription factors that
XX PT interact with them - for control of apoptosis, e.g. in treatment of
XX PT cancer, viral infection, neurodegeneration and autoimmune disease.
XX PS Claim 1; Page 38; 60pp; English.
XX CC This sequence represents a regulatory region from the CD95 gene, and is a
XX CC nucleic acid of the invention. The regulatory regions (silencers or
XX CC enhancers) are involved in apoptosis, i.e. inhibition of CD95 expression
XX CC will inhibit apoptosis. Regulation of apoptosis is useful in treatment of
XX CC cancer, (retroviral infection, neurodegeneration and autoimmune disease,
XX CC e.g. by gene therapy for expressing transcription factors or expression
XX CC of antisense sequences to inhibit transcription factor production. The
XX CC regulatory nucleic acids and transcription factors are also useful for
XX CC studying regulation of CD95 in vitro or in vivo, to screen for modulators
XX CC and as probes to isolate related genes
XX SQ Sequence 28 BP; 8 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28
Db 28 GTCTGGAACTGCATCCAAATTCAGGTTTC 1

RESULT 3
ABK88709/c
ID ABK88709 standard; DNA; 28 BP.
XX SQ Sequence 28 BP; 8 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28
Db 28 GTCTGGAACTGCATCCAAATTCAGGTTTC 1

RESULT 4
ABK88700
ID ABK88700 standard; DNA; 28 BP.
XX SQ Sequence 28 BP; 8 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28
Db 28 GTCTGGAACTGCATCCAAATTCAGGTTTC 1

RESULT 4
ABK88700
ID ABK88700 standard; DNA; 28 BP.
XX
```

```

XX AC ABK88709;
XX DT 07-OCT-2002 (first entry)
XX DE Human CD95 gene transcription silencer probe #1.
XX KW Human; apoptotic cell death; proteinaceous transcription factor;
XX KW regulation of gene transcription; apoptosis; p53; CD95; TRA;
XX KW transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;
XX KW tumour cell; embryonic cell; nervous system; intracellular pathogen;
XX KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;
XX KW immune system dysfunction; anti-tumour; cytostatic; hCD95;
XX KW transcription silencer region; probe; ss.
XX OS Homo sapiens.
XX PN WO200244363-A1.
XX PD 06-JUN-2002.
XX PF 28-NOV-2001; 2001WO-NZ000287.
XX PR 28-NOV-2000; 2000US-00724809.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Lasham A, Watson JD;
XX DR WPI; 2002-557540/59.
XX PT Modulating p53-mediated apoptotic cell death in a population of cells, by
XX PT modulating the amount of a transcriptional regulator of apoptosis
XX PS Example 1; Page 54; 62pp; English.
XX CC The present invention relates to methods for modulating apoptotic cell
XX CC death using proteinaceous transcription factors that regulate the
XX CC transcription of genes encoding proteins involved in apoptosis (e.g. CD95
XX CC and p53). The methods involve modulating the amount of a transcriptional
XX CC regulator of apoptosis (TRA) available to bind to a target polynucleotide
XX CC in the cells, where TRA is a member of the Y-box nucleic acid binding
XX CC family of polypeptides (e.g. YB-1). The methods of the invention are
XX CC useful for modulating apoptotic cell death in a population of cells,
XX CC where the cells are selected from tumour cells, cells of the immune
XX CC system, embryonic cells, cells of the nervous system, or cells infected
XX CC with intracellular pathogens. The methods are also useful for increasing
XX CC the sensitivity of tumour cells to a DNA-damaging agent, and for
XX CC increasing sensitivity to apoptosis in a population of cells harbouring
XX CC intracellular pathogens. The methods are useful for screening an
XX CC apoptosis modulatory agent that modulates the binding of TRA. The methods
XX CC for regulating apoptosis can be used therapeutically and prophylactically
XX CC for various disorders such as cancer, viral and retroviral infections,
XX CC neurodegenerative disorders, and immune system dysfunction. The present
XX CC sequence represents a human CD95 (hCD95) gene transcription silencer
XX CC probe
XX SQ Sequence 28 BP; 8 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28
Db 28 GTCTGGAACTGCATCCAAATTCAGGTTTC 1

RESULT 4
ABK88700
ID ABK88700 standard; DNA; 28 BP.
XX
```


AC ABK88700;
XX
XX
DT 07-OCT-2002 (first entry)
XX
DE Transcription silencer region (S1) of human CD95 gene.
XX
XX Human; apoptotic cell death; proteinaceous transcription factor;
KW regulation of gene transcription; apoptosis; p53; CD95; TRA;
KW transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;
KW tumour cell; embryonic cell; nervous system; intracellular pathogen;
KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;
KW immune system dysfunction; anti-tumour; cytostatic; S1; hCD95;
KW transcription silencer region; ds.
XX
XX Homo sapiens.
OS
XX WO200244363-A1.
PN
XX
XX
PD 06-JUN-2002.
XX
XX
PF 28-NOV-2001; 2001WO-NZ000287.
XX
XX 28-NOV-2000; 2000US-00724809.
PR
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
XX Lasham A, Watson JD;
PI
XX WPI; 2002-557540/59.
DR
XX
XX Modulating p53-mediated apoptotic cell death in a population of cells, by
PT modulating the amount of a transcriptional regulator of apoptosis
PT available to bind to a target polynucleotide in the cells.
PT
XX
PS Example 1; Page 53; 62pp; English.
XX
XX The present invention relates to methods for modulating apoptotic cell
CC death using proteinaceous transcription factors that regulate the
CC transcription of genes encoding proteins involved in apoptosis (e.g. CD95
CC and p53). The methods involve modulating the amount of a transcriptional
CC regulator of apoptosis (TRA) available to bind to a target polynucleotide
CC in the cells, where TRA is a member of the Y-box nucleic acid binding
CC family of polypeptides (e.g. YB-1). The methods of the invention are
CC useful for modulating apoptotic cell death in a population of cells,
CC where the cells are selected from tumour cells, cells of the immune
CC system, embryonic cells, cells of the nervous system, or cells infected
CC with intracellular pathogens. The methods are also useful for increasing
CC the sensitivity of tumour cells to a DNA-damaging agent, and for
CC increasing sensitivity to apoptosis in a population of cells harbouring
CC intracellular pathogens. The methods are useful for screening an
CC apoptosis modulatory agent that modulates the binding of TRA. The methods
CC for regulating apoptosis can be used therapeutically and prophylactically
CC for various disorders such as cancer, viral and retroviral infections,
CC neurodegenerative disorders, and immune system dysfunction. The present
CC sequence represents the transcription silencer region (S1) of the human
CC CD95 (hcd95) gene
XX
XX Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCGTGAAGTGCATCCAAATTCAGGTTTC 28
DB 1 GTCGTGAAGTGCATCCAAATTCAGGTTTC 28

RESULT 5
AAV23172
ID AAV23172 standard; DNA; 50 BP.
XX
XX AAV23172;
AC

XX 23-JUL-1998 (first entry)
DT
XX
DE CD95 enhancer binding site.
XX
XX CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;
KW cancer; viral infection; neurodegeneration; autoimmune disease;
KW gene therapy; transcription factor; ss.
XX
OS Homo sapiens.
XX
XX WO9808965-A2.
PN
XX
XX 05-MAR-1998.
PD
XX
XX 29-AUG-1997; 97WO-NZ000107.
PF
XX
XX 30-AUG-1996; 96US-00713557.
PR
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
XX Watson JD, Rudert F;
PI
XX WPI; 1998-179445/16.
DR
XX
XX New regulatory regions from the CD95 gene and transcription factors that
PT interact with them - for control of apoptosis, e.g. in treatment of
PT cancer, viral infection, neurodegeneration and autoimmune disease.
XX
XX Disclosure; Page 43; 60pp; English.
PS
XX This sequence represents a regulatory region from the CD95 gene, and is a
CC nucleic acid of the invention. The regulatory regions (silencers or
CC enhancers) are involved in apoptosis, i.e. inhibition of CD95 expression
CC will inhibit apoptosis. Regulation of apoptosis is useful in treatment of
CC cancer, (retro)viral infection, neurodegeneration and autoimmune disease,
CC e.g. by gene therapy for expressing transcription factors or expression
CC of antisense sequences to inhibit transcription factor production. The
CC regulatory nucleic acids and transcription factors are also useful for
CC studying regulation of CD95 in vitro or in vivo, to screen for modulators
CC and as probes to isolate related genes
XX
XX Sequence 50 BP; 16 A; 10 C; 10 G; 14 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 28; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCGTGAAGTGCATCCAAATTCAGGTTTC 28
DB 1 GTCGTGAAGTGCATCCAAATTCAGGTTTC 28

RESULT 6
AAT34162
ID AAT34162 standard; DNA; 1608 BP.
XX
XX AAT34162;
AC
XX
XX 22-OCT-1996 (first entry)
DT
XX Fas promoter region.
DE
XX Fas gene promoter; apoptosis; ageing; autoimmune disease;
KW T-cell senescence; ss.
XX
XX Homo sapiens.
OS
XX
XX Key
FT promoter
FT /tag= a
FT /note= "Fas gene promoter region"
FT protein_bind 147.151

FT /tag= b
 FT /function= "GFI transcription factor binding site"
 FT /note= "Claim 7"
 FT protein_bind 168. .174
 FT /tag= c
 FT /function= "ESP20 transcription factor binding site"
 FT protein_bind 272. .276
 FT /tag= d
 FT /function= "Myb transcription factor binding site"
 FT /note= "Claim 9"
 FT protein_bind 349. .353
 FT /tag= e
 FT /function= "NF-Y transcription factor binding site"
 FT protein_bind 521. .525
 FT /tag= f
 FT /function= "GF-1 transcription factor binding site"
 FT /note= "Claim 7"
 FT protein_bind 604. .609
 FT /tag= g
 FT /function= "NF-Y transcription factor binding site"
 FT /note= "Claim 8"
 FT protein_bind 621. .626
 FT /tag= h
 FT /function= "AP-1 transcription factor binding site"
 FT /note= "Claim 5"
 FT protein_bind 1037. .1043
 FT /tag= i
 FT /function= "CP2 transcription factor binding site"
 FT /note= "Claim 6"
 FT exon 1075. .1476
 FT /tag= j
 FT /codon_start= 1479. .1469
 FT /product= "Fas protein leader"
 FT intron 1497. .1608
 FT /tag= j
 FT /note= "5' end of intron 1 (full length approx. 14 kb)"
 FT XX
 FT WO9622370-A1.
 FT XX
 FT 25-JUL-1996.
 FT PD XX
 FT 19-JAN-1996; 96WO-US000606.
 FT PF XX
 FT 20-JAN-1995; 95US-00377522.
 FT PR XX
 FT (UABR-) UAB RES FOUND.
 FT PA XX
 FT Mountz JD, Liu C, Cheng J, Koopman WJ, Zhou T;
 FT PI XX
 FT WPI; 1996-354527/35.
 FT DR P-PSDB; AAR39471.
 FT XX
 FT Human Fas gene promoter region - used for heterologous protein expression
 FT PT and for developing products for treating Fas-mediated apoptosis
 FT PT disorders.
 FT XX
 FT Claim 11; Fig 2; 123pp; English.
 FT PS
 FT A novel DNA segment (AAR34162) has an isolated sequence region defined as
 FT CC the Fas gene promoter region. This includes a number of transcription
 FT CC factor binding sites. A coding sequence for the N-terminal portion
 FT CC (AAR39471) of the Fas protein leader peptide is also included. The DNA
 FT CC segment was isolated from a human placental DNA library using a 32p-
 FT CC labeled segment of human Fas cDNA corresponding to nt 23-346. It can be
 FT CC combined with a structural gene so that the gene is under the
 FT CC transcriptional control of the transcription factor binding sites. The
 FT CC promoter region can be used to regulate Fas gene expression. e.g. in
 FT CC tumour or immune cells, as a means of treating Fas-mediated apoptosis
 FT CC disorders such as malignancies and autoimmune diseases
 FT XX
 FT Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 1608;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCTGGAAGTGCATCCAAATTCAGGTTTC 28
 Db 433 GTCTGGAAGTGCATCCAAATTCAGGTTTC 460
 RESULT 7
 ABN79677
 ID ABN79677 standard; DNA; 2165 BP.
 XX
 AC ABN79677;
 XX
 DT 29-JUL-2002 (first entry)
 XX
 DE Sequence #1 used to generate target oligonucleotides.
 XX
 KW Human; immunosuppressive; antiinflammatory; hepatotropic; cytostatic;
 KW vasotropic; hepatitis; cancer; allograft rejection; ds; Fas.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1782..1813
 FT /tag= a
 FT /product= "peptide encoded by sequence used create target
 FT oligonucleotides"
 XX
 PN US2002004490-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 09-MAR-2001; 2001US-00802669.
 PR 12-APR-1999; 99US-00290640.
 PR 18-SEP-2000; 2000US-00665615.
 XX
 PA (DEAN/) DEAN N M.
 PA (MARC/) MARCUSSEN E G.
 PA (WYAT/) WYATT J.
 PA (ZHAN/) ZHANG H.
 XX
 PI Dean NM, Marcussen EG, Wyatt J, Zhang H;
 XX
 DR WPI; 2002-204886/26.
 DR P-PSDB; ABP35566.
 XX
 PT Novel antisense compound targeted to nucleic acid encoding Fas, Fas
 PT ligand or Fas associated protein-1 is useful for inhibiting expression of
 PT Fas, Fas ligand, or Fas-1 in cells or tissues, and for treating
 PT hepatitis.
 XX
 PS Example 18; Page 62-63; 84pp; English.
 XX
 CC This invention relates to an antisense compound encoding Fas, Fas ligand,
 CC or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated
 CC signalling is thought to be immunosuppressive, antiinflammatory,
 CC hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were
 CC designed to target human Fas. Oligonucleotides were synthesised as
 CC chimeric oligonucleotides and are useful for treating an animal having an
 CC autoimmune or inflammatory disease e.g. hepatitis, cancer, a condition
 CC associated with apoptosis, allograft rejection, or ischemia reperfusion
 CC injury. Optionally, the above mentioned conditions are prevented by
 CC contacting the allograft with the antisense oligonucleotide. The
 CC oligonucleotides are used in diagnostics, therapeutics, prophylaxis and
 CC as research reagents and in kits. The oligonucleotides are also useful
 CC for research purposes. The present nucleotide sequence is related to
 CC human Fas
 XX
 SQ Sequence 2165 BP; 508 A; 555 C; 555 G; 547 T; 0 U; 0 Other;

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Query Match      100.0%; Score 28; DB 6; Length 2165;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
Db 747 GTCGGAAGTGCATCCAAATTCAGGTTTC 774

RESULT 8
ADE43798
ID ADE43798 standard; DNA; 28118 BP.
XX
XX AC
XX ADE43798;
XX
XX 29-JAN-2004 (first entry)
XX
XX Polymorphic human TNFRSF6 genomic sequence, SEQ ID 403.
XX
XX Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW Chromosome 10; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 199
FT /tag= a
FT /note= "There is a variation at this position"
FT 213
FT /tag= b
FT /note= "There is a variation at this position"
FT 843
FT /tag= c
FT /note= "There is a variation at this position"
FT 1530
FT /tag= d
FT /note= "There is a variation at this position"
FT 1550
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FT /note= "There is a variation at this position"
FT 2967
FT /tag= f
FT /note= "There is a variation at this position"
FT 3103
FT /tag= g
FT /note= "There is a variation at this position"
FT 5335
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FT /note= "There is a variation at this position"
FT 5345
FT /tag= i
FT /note= "There is a variation at this position"
FT 6074
FT /tag= j
FT /note= "There is a variation at this position"
FT 9374
FT /tag= k
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FT 9907
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FT 9936
FT /tag= m
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FT 10937
FT /tag= n
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FT 11200
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FT 11279
FT /tag= p
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FT /note= "There is a variation at this position"
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FT 11503
FT /tag= r
FT /note= "There is a variation at this position"
FT 11511
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FT /note= "There is a variation at this position"
FT 11587
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FT 11694
FT /tag= u
FT /note= "There is a variation at this position"
FT 11905
FT /tag= v
FT /note= "There is a variation at this position"
FT 12193
FT /tag= w
FT /note= "There is a variation at this position"
FT 12208
FT /tag= x
FT /note= "There is a variation at this position"
FT 12238
FT /tag= y
FT /note= "There is a variation at this position"
FT 14525
FT /tag= z
FT /note= "There is a variation at this position"
FT 14714
FT /tag= aa
FT /note= "There is a variation at this position"
FT 18511
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FT 18567
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FT 18982
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FT 19069
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FT 20412
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FT 20552
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FT 21585
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FT 22439
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FT 23199
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FT 23416
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FT 24890
FT /tag= am
FT /note= "There is a variation at this position"
FT 26359
FT /tag= an
FT /note= "There is a variation at this position"
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XX WO2003054143-A2.
 XX PD 03-JUL-2003.
 XX PF 25-OCT-2002; 2002WO-US034679.
 XX PR 25-OCT-2001; 2001US-0339525P.
 XX PR 08-NOV-2001; 2001US-0336929P.
 XX PR 08-NOV-2001; 2001US-0338010P.
 XX PR 09-NOV-2001; 2001US-0338363P.
 XX PR 04-DEC-2001; 2001US-0337052P.
 XX PR 28-MAR-2002; 2002US-0368919P.
 XX PA (NEUR-) NEUROGENETICS INC.
 XX PA (GHEO) GEN HOSPITAL CORP.
 XX PI Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
 XX PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
 XX DR WPI; 2003-559131/52.
 XX PT Determining a predisposition for or the occurrence of neurodegenerative
 XX PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
 XX PT the presence or absence of an allelic variant of one or more polymorphic
 XX PT regions.
 XX PS Claim 12; Page 699-707; 848pp; English.
 XX CC The present invention relates to a method (M1) for determining a
 XX CC predisposition for or the occurrence of neurodegenerative disease in a
 XX CC subject. The method comprises detecting in a target nucleic acid obtained
 XX CC from the subject the presence or absence of an allelic variant of one or
 XX CC more polymorphic regions of one or more genes selected from UPA
 XX CC (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
 XX CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
 XX CC lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
 XX CC presence of at least one of the allelic variant of one or more
 XX CC polymorphic regions is indicative of a predisposition for or the
 XX CC occurrence of neurodegenerative disease. The genes are all located on
 XX CC chromosome 10. M1 is useful for determining a predisposition for or the
 XX CC occurrence of, and for treating neurodegenerative disease, particularly
 XX CC Alzheimer's disease.
 XX SQ Sequence 28118 BP; 8375 A; 5380 C; 5368 G; 8952 T; 0 U; 43 Other;
 Query Match 100.0%; Score 28; DB 9; Length 28118;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCTGGAATCGATCCAAATTCAGGTTTC 28
 Db 1186 GTCTGGAATCGATCCAAATTCAGGTTTC 1213
 RESULT 9
 AD243797
 ID ADE43797 standard; DNA; 28118 BP.
 XX AC ADE43797;
 XX AC ADE43797;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human TNFRSF6 genomic sequence, SEQ ID 402.
 XX KW Neurodegenerative disease; UPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
 XX KW Alzheimer's disease; neuroprotective; neurotropic; gene therapy;
 XX KW Chromosome 10; gene; ds.
 XX OS Homo sapiens.
 XX PN WO2003054143-A2.
 XX PF 26-DEC-2002; 2002WO-US041414.

PD 03-JUL-2003.
 XX PF 25-OCT-2002; 2002WO-US034679.
 XX PR 25-OCT-2001; 2001US-0339525P.
 XX PR 08-NOV-2001; 2001US-0336929P.
 XX PR 08-NOV-2001; 2001US-0338010P.
 XX PR 09-NOV-2001; 2001US-0338363P.
 XX PR 04-DEC-2001; 2001US-0337052P.
 XX PR 28-MAR-2002; 2002US-0368919P.
 XX PA (NEUR-) NEUROGENETICS INC.
 XX PA (GHEO) GEN HOSPITAL CORP.
 XX PI Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
 XX PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
 XX DR WPI; 2003-559131/52.
 XX PT Determining a predisposition for or the occurrence of neurodegenerative
 XX PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
 XX PT the presence or absence of an allelic variant of one or more polymorphic
 XX PT regions.
 XX PS Claim 25; Page 691-699; 848pp; English.
 XX CC The present invention relates to a method (M1) for determining a
 XX CC predisposition for or the occurrence of neurodegenerative disease in a
 XX CC subject. The method comprises detecting in a target nucleic acid obtained
 XX CC from the subject the presence or absence of an allelic variant of one or
 XX CC more polymorphic regions of one or more genes selected from UPA
 XX CC (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
 XX CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
 XX CC lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
 XX CC presence of at least one of the allelic variant of one or more
 XX CC polymorphic regions is indicative of a predisposition for or the
 XX CC occurrence of neurodegenerative disease. The genes are all located on
 XX CC chromosome 10. M1 is useful for determining a predisposition for or the
 XX CC occurrence of, and for treating neurodegenerative disease, particularly
 XX CC Alzheimer's disease.
 XX SQ Sequence 28118 BP; 8387 A; 5390 C; 5378 G; 8963 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 9; Length 28118;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCTGGAATCGATCCAAATTCAGGTTTC 28
 Db 1186 GTCTGGAATCGATCCAAATTCAGGTTTC 1213
 RESULT 10
 ADA02744
 ID ADA02744 standard; DNA; 45121 BP.
 XX AC ADA02744;
 XX AC ADA02744;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human TNFRSF6 carcinoma associated gene, SEQ ID NO:1262.
 XX KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
 XX KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
 XX KW gene; ds.
 XX OS Homo sapiens.
 XX PN WO2003057146-A2.
 XX PD 17-JUL-2003.
 XX PF 26-DEC-2002; 2002WO-US041414.

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XX PR 26-DEC-2001; 2001US-00035832.
XX PA (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW;
XX DR WPI; 2003-587068/55.
XX PT New recombinant nucleic acid encoding carcinoma associated protein,
XX PT useful for preparing compositions for treating carcinomas.
XX PS Claim 1; SEQ ID NO 1262; 245pp; English.
XX CC The invention relates to recombinant carcinoma associated (CA) nucleic
XX CC acid sequences from mouse and human (ADA01482-ADA03094), and to
XX CC recombinant carcinoma associated proteins (CAP) encoded by them. The
XX CC invention also encompasses expression vectors and host cells comprising a
XX CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
XX CC binds to the protein, and a biochip comprising CA nucleic acid or
XX CC fragments thereof. The sequences of the invention were identified using
XX CC oncogenic retroviruses, which insert into the genome of the host organism
XX CC at random. Many of these do not carry transduced host oncogenes or
XX CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
XX CC direct consequence of the effects of proviral integration into host
XX CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
XX CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
XX CC leukaemia) or a propensity to carcinoma by determination of the sequence
XX CC of a CA gene, or by determination of CA gene expression in particular
XX CC tissues. CA nucleic acids, proteins and antibodies are also useful as
XX CC therapeutic agents and in screening and evaluating drug candidates. The
XX CC present sequence represents a specifically claimed human CA nucleic acid
XX CC sequence of the invention. Note: The complete sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 45121 BP; 13226 A; 8836 C; 9010 G; 14049 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 8; Length 45121;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGTGGAAGTCATCCAAATTCAGGTTC 28
DB 9186 GTCGTGGAAGTCATCCAAATTCAGGTTC 9213

RESULT 11
ADB72482
ID ADB72482 standard; DNA; 45121 BP.
AC ADB72482;
DT 04-DEC-2003 (first entry)
DE Human TNFRSF6 gene.
KW human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.
OS Homo sapiens.
XX WO2003008583-A2.
XX PN 30-NOV-2001; 2001US-00097722.
XX PD 30-JAN-2003.
XX PF 26-DEC-2001; 2001WO-US051291.
XX PR 02-MAR-2001; 2001US-00798586.
XX PR 23-OCT-2001; 2001US-00004113.
XX PR 08-NOV-2001; 2001US-00052482.
XX PR 30-NOV-2001; 2001US-00997722.

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PR 20-DEC-2001; 2001US-00034650.
XX (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW, Engelhard EK;
XX DR WPI; 2003-239337/23.
XX PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
XX PT cancers, neoplasm, adenocarcinoma, or sarcomas.
XX PS Claim 1; SEQ ID NO 310; 2304pp; English.
XX CC The invention relates to a novel recombinant nucleic acid comprising a
XX CC nucleotide sequence selected from any of the 660 sequences fully defined
XX CC in the specification. A polynucleotide of the invention has cytostatic
XX CC activity, and may have a use in gene therapy, or in a vaccine. The
XX CC recombinant nucleic acids and polypeptides are useful for treating
XX CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
XX CC sarcomas. The present sequence represents a human gene of the invention.
XX SQ Sequence 45121 BP; 13226 A; 8836 C; 9010 G; 14049 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 9; Length 45121;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGTGGAAGTCATCCAAATTCAGGTTC 28
DB 9186 GTCGTGGAAGTCATCCAAATTCAGGTTC 9213

RESULT 12
ADC85224
ID ADC85224 standard; DNA; 45121 BP.
XX AC ADC85224;
XX DT 01-JAN-2004 (first entry)
XX DE Human TNFRSF6 genomic sequence.
XX KW Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;
XX KW secreted; transmembrane; intracellular; ds.
XX OS Homo sapiens.
XX PN WO2003045230-A2.
XX PD 05-JUN-2003.
XX PF 02-DEC-2002; 2002WO-US038582.
XX PR 30-NOV-2001; 2001US-00997722.
XX (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW, Engelhard EK;
XX DR WPI; 2003-513603/48.
XX PT New recombinant nucleic acid comprising a nucleotide sequence of any of
XX PT the carcinoma-associated (CA) genes, useful for screening for drug
XX PT candidates for diagnosing or treating carcinomas.
XX PS Claim 1; SEQ ID NO 10; 983pp; English.
XX CC The invention relates to a recombinant nucleic acid comprising a
XX CC nucleotide sequence selected from any of the fully defined carcinoma-
XX CC associated (CA) genes from the 50 tables given in the specification. The
XX CC CA proteins are secreted, transmembrane or intracellular proteins. The
XX CC recombinant nucleic acids are useful for screening for drug candidates
XX CC for diagnosing or treating carcinomas. Sequences given in ADC85215-

```

CC ADC85514 represent CA genes of the invention.

XX Sequence 45121 BP; 13226 A; 8836 C; 9010 G; 14049 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 28; DB 9; Length 45121;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTGCATCCAAATTCAGGTTTC 28
DB 9186 GTCTGGAAGTGCATCCAAATTCAGGTTTC 9213

RESULT 13

RAD46346/c

ID AAD46346 standard; DNA; 9193 BP.

XX AAD46346;

AC AAD46346;

XX 27-JAN-2003 (first entry)

DT Human nuclear receptor L67 gene.

DE Human; nuclear receptor; L67; metabolic disorder; hormonal dysfunction;
XX immunological; cellular defence mechanism; immunomodulator; cytostatic;
KW arteriosclerosis; cell proliferation; neurosystemic disease; therapy;
KW cell aberration; cholesterol; differentiation; receptor; gene; ds.

XX Homo sapiens.

OS WO200270697-A1.

XX 12-SEP-2002.

PF 21-FEB-2002; 2002WO-EP001864.

XX 02-MAR-2001; 2001EP-00105098.

PA (LION-) LION BIOSCIENCE AG.

XX Casari G, Jackson D, Suckow J;

XX WPI; 2002-723265/78.

XX New nuclear receptor (L67) nucleic acids and proteins, useful for
PT developing and identifying compounds for treating disorders of cell
PT metabolism, homeostasis, proliferation and differentiation.

XX Claim 1; Page 52-57; 67pp; English.

XX The invention relates to nuclear receptor (L67) nucleic acids, proteins
CC and methods of use of L67 receptor. L67 is useful in identifying agents
CC that inhibit its cellular function. The method is useful for inhibiting
CC the cellular function of L67. The invention is useful for developing and
CC identifying compounds for treating metabolic disorders, hormonal
CC dysfunctions, immunological indications, neurosystemic diseases, high
CC cholesterol, or arteriosclerosis. L67 DNA is useful for making vectors
CC and for transforming cell that can be used for producing L67 protein. It
CC is also useful as scientific research tools for developing nucleic acid
CC probes for determining L67 expression levels, e.g. to identify disease or
CC abnormal states. It can also be used for developing analytical tools such
CC as antisense oligonucleotides for selectively inhibiting expression of
CC the L67 gene to determine physiological responses. L67 is useful for
CC screening for L67 antagonist and agonist activity for controlling
CC cellular functions such as cell proliferation, differentiation,
CC aberrations or cellular defence mechanisms. The present sequence is human
CC L67 gene

XX Sequence 9193 BP; 2535 A; 2255 C; 2013 G; 2390 T; 0 U; 0 Other;

XX Query Match 71.4%; Score 20; DB 6; Length 9193;

XX Best Local Similarity 82.1%; Pred. No. 70;

XX Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTGCATCCAAATTCAGGTTTC 28
DB 1221 GTCTGGAAGTGCATCCAAATTCAGGTTTC 1194

RESULT 14

ABL34419/c

ID ABL34419 standard; DNA; 1608 BP.

XX ABL34419;

XX 26-MAR-2002 (first entry)

DE Human immune system associated gene SEQ ID NO: 2392.

XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; neutropenic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
ds.

XX Homo sapiens.

OS WO200200928-A2.

XX 03-JAN-2002.

PF 02-JUL-2001; 2001WO-EP007537.

XX 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

XX Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention

XX Sequence 1608 BP; 366 A; 51 C; 421 G; 770 T; 0 U; 0 Other;

XX Query Match 67.9%; Score 19; DB 6; Length 1608;

XX Best Local Similarity 81.5%; Pred. No. 1.5e+02;

XX Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAAGTGCATCCAAATTCAGGTTTC 28

DB 1175 TCTAAGTGCATCCAAATTCAGGTTTC 1149

RESULT 15

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ID ADAL3316 standard; DNA; 108359 BP.

XX ADAL3316;

[illegible]

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FT               /note= "Single nucleotide polymorphism (SNP)"
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FT               /note= "Single nucleotide polymorphism (SNP)"
FT variation      replace(36567,A)
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FT               /note= "Single nucleotide polymorphism (SNP)"
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FT               /*tag= az
FT               /note= "Single nucleotide polymorphism (SNP)"
FT variation      replace(37852,A)
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FT               /note= "Single nucleotide polymorphism (SNP)"
FT variation      replace(39945,A)
FT               /*tag= bc
FT               /note= "Single nucleotide polymorphism (SNP)"
FT variation      replace(41831,T)
FT               /*tag= bd
FT               /note= "Single nucleotide polymorphism (SNP)"
FT exon           43036. .43099
FT               /*tag= be
FT intron         43100. .48332
FT               /*tag= bf
FT variation      replace(43425,A)
FT               /*tag= bg
FT               /note= "Single nucleotide polymorphism (SNP)"
FT variation      replace(43806,T)
FT               /*tag= bh
FT               /note= "Single nucleotide polymorphism (SNP)"
FT exon           48333. .48452
FT               /*tag= bi
FT intron         48453. .50526
FT               /*tag= bj
FT variation      replace(49219,C)
FT               /*tag= bk
FT               /note= "Single nucleotide polymorphism (SNP)"
FT variation      replace(49259,A)

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Query Match      67.9%; Score 19; DB 8; Length 108359;
Best Local Similarity 81.5%; Pred. No. 3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 2 TCTGGAACTGCATCCAAATTCAGGTTTC 28
Db 49691 TCTGGAACTGCAAACAATTACGATTC 49665

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Search completed: September 1, 2004, 20:55:46
Job time : 236 secs

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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 17:48:16 ; Search time 47 Seconds
(without alignments)
330.609 Million cell updates/sec

Title: US-10-028-415-2

Perfect score: 28
Sequence: 1 gctgggaactgcattcaaatccaggttc 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	28	100.0	28	2	US-08-713-557B-2
2	28	100.0	28	2	US-08-713-557B-14
3	28	100.0	50	2	US-08-713-557B-35
4	28	100.0	2165	4	US-09-686-615B-94
5	17.4	62.1	572	1	US-08-253-155A-15
6	17.4	62.1	1250	4	US-09-023-655-580
7	17.4	62.1	4403785	3	US-09-103-840A-2
8	17.4	62.1	4411529	3	US-09-103-840A-1
9	17.2	61.4	291	4	US-09-540-236-395
10	17.2	61.4	1647	4	US-09-540-236-415
11	17.2	61.4	92407	4	US-09-596-002-36
12	17	60.7	305	4	US-09-313-294A-4746
13	17	60.7	483	4	US-09-328-352-2611
14	17	60.7	722	3	US-08-480-640A-222
15	17	60.7	722	3	US-08-686-968C-222
16	17	60.7	722	3	US-08-488-237A-222
17	17	60.7	722	4	US-08-472-679H-222
18	17	60.7	794	4	US-09-173-300-10
19	17	60.7	3164	3	US-08-686-968C-1
20	17	60.7	12619	4	US-09-616-289-49
21	17	60.7	13187	4	US-09-422-936-61
22	17	60.7	50000	4	US-09-146-053-4
23	17	60.7	65042	4	US-09-784-316-3
24	16.8	60.0	2496	1	US-08-073-384C-2
25	16.8	60.0	2496	1	US-08-254-359A-2
26	16.8	60.0	2496	1	US-08-483-043-2
27	16.8	60.0	2496	1	US-08-481-238-2

28	16.8	60.0	2496	2	US-08-471-066B-2	Sequence 2, Appli
29	16.8	60.0	2496	2	US-08-484-956-2	Sequence 2, Appli
30	16.8	60.0	2496	2	US-08-757-653-2	Sequence 2, Appli
31	16.8	60.0	2496	2	US-08-599-491-2	Sequence 2, Appli
32	16.8	60.0	2496	2	US-08-756-386-2	Sequence 2, Appli
33	16.8	60.0	2496	2	US-08-823-516-2	Sequence 2, Appli
34	16.8	60.0	2496	3	US-08-682-853A-2	Sequence 2, Appli
35	16.8	60.0	2496	3	US-08-759-038-2	Sequence 2, Appli
36	16.8	60.0	2496	3	US-08-758-314-2	Sequence 2, Appli
37	16.8	60.0	2496	4	US-09-350-303-2	Sequence 2, Appli
38	16.8	60.0	2496	4	US-08-520-946-2	Sequence 2, Appli
39	16.8	60.0	2496	4	US-09-684-938-2	Sequence 2, Appli
40	16.8	60.0	2496	4	US-09-308-825A-2	Sequence 2, Appli
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42	16.8	60.0	2496	4	US-09-655-378A-2	Sequence 2, Appli
43	16.8	60.0	2850	4	US-09-620-312D-125	Sequence 125, App
44	16.8	60.0	197496	4	US-09-877-177A-10	Sequence 10, Appli
45	16.6	59.3	2493	3	US-08-945-056-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-713-557B-2
; Sequence 2, Application US/08713557B
; Patent No. 5912168
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Rudert, Fritz
; TITLE OF INVENTION: CD95 REGULATORY GENE SEQUENCES
; TITLE OF INVENTION: AND TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 30-AUG-1996
; APPLICATION NUMBER: US/08/713,557B
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Speckman, Ann W
; REGISTRATION NUMBER: 31,881
; REFERENCE/DOCKET NUMBER: 11000.1004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-713-557B-2

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00026; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;
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Db 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
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RESULT 2
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; Sequence 14, Application US/08713557B
; Patent No. 5912168
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Rudert, Fritz
; TITLE OF INVENTION: CD95 REGULATORY GENE SEQUENCES
; TITLE OF INVENTION: AND TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,557B
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Speckman, Ann W
; REGISTRATION NUMBER: 31,881
; REFERENCE/DOCKET NUMBER: 11000.1004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-713-557B-35
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Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
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RESULT 4
US-09-665-615B-94
; Sequence 94, Application US/09665615B
; Patent No. 6653133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-665-615B-94
Query Match 100.0%; Score 28; DB 4; Length 2165;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
|||||
Db 747 GTCGGAAGTGCATCCAAATTCAGGTTTC 774
|||||
```

RESULT 5
US-08-253-155A-15
; Sequence 15, Application US/08253155A
; Patent No. 5691147
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: CDK4 Binding Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,155A
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 572 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-253-155A-15

Query Match 62.1%; Score 17.4; DB 1; Length 572;
Best Local Similarity 77.8%; Pred. No. 55;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TCTGGAACGTCATCCAAATTCAGGTC 28
Db 348 TCTGGAACGCTCCAACTGCAGGCTC 374

RESULT 6
US-09-023-655-580
; Sequence 580, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 62.1%; Score 17.4; DB 1; Length 572;
Best Local Similarity 77.8%; Pred. No. 55;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TCTGGAACGTCATCCAAATTCAGGTC 28
Db 348 TCTGGAACGCTCCAACTGCAGGCTC 374

RESULT 7
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007-00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 62.1%; Score 17.4; DB 3; Length 4403765;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TCTGGAACGTCATCCAAATTCAGGTC 28
Db 330484 TCTGAATCTGAATCTAATCAATCAGGTC 330458

RESULT 8
US-09-103-840A-1/c

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; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 62.1%; Score 17.2; DB 3; Length 4411529;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TCTGGAATCATCAAAATTCAGGTTTC 28
DB 330375 TCTGAATCTGAATCTAATCAATCAGGTTTC 330349

RESULT 9
US-09-540-236-395/c
; Sequence 395, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 395
; LENGTH: 291
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-395

Query Match 61.4%; Score 17.2; DB 4; Length 291;
Best Local Similarity 86.4%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GAACTGCATCCAAATTCAGGTT 27
DB 266 GAAATGCATCCAGCTTCAGGTT 245

RESULT 10
US-09-540-236-415
; Sequence 415, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 415
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: M.catarrhalis

US-09-540-236-415
Query Match 61.4%; Score 17.2; DB 4; Length 1647;
Best Local Similarity 86.4%; Pred. No. 88;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GAACTGCATCCAAATTCAGGTT 27
DB 1399 GAAATGCATCCAGCTTCAGGTT 1420

RESULT 11
US-09-596-002-36
; Sequence 36, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 92407
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 36
; PUBLICATION INFORMATION:
US-09-596-002-36

Query Match 61.4%; Score 17.2; DB 4; Length 92407;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GAACTGCATCCAAATTCAGGTT 27
DB 68664 GAAATGCATCCAGCTTCAGGTT 68685

RESULT 12
US-09-313-294A-4746/c
; Sequence 4746, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Ialugudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4746
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700348970H1
; NAME/KEY: unsure
; LOCATION: 47
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4746

Query Match 60.7%; Score 17; DB 4; Length 305;
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Best Local Similarity 80.0%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTGCATCCAAATTCAGG 25
Db 107 GTCATGAACAGCATCCAAATAAAGG 83

RESULT 13
US-09-328-352-2611/C
; Sequence 2611, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC98-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; SEQ ID NO 2611
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2611

Query Match 60.7%; Score 17; DB 4; Length 483;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAAGTGCATCCAAATTCAGGT 26
Db 89 TCTGGAAGTGCATCCAAATTCAGGT 65

RESULT 14
US-08-480-640A-222
; Sequence 222, Application US/08480640A
; Patent No. 6033904
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,640A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 222:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-640A-222

Query Match 60.7%; Score 17; DB 3; Length 722;
Best Local Similarity 80.0%; Pred. No. 90;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAAGTGCATCCAAATTCAGGT 26
Db 625 TATGGAACAGCATCCCAATTCAGAT 649

RESULT 15
US-08-686-968C-222
; Sequence 222, Application US/08686968C
; Patent No. 6221361
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; FILE REFERENCE: 39119-H/JML
; CURRENT APPLICATION NUMBER: US/08/686,968C
; CURRENT FILING DATE: 1996-07-25
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 222
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Swinepox virus
US-08-686-968C-222

Query Match 60.7%; Score 17; DB 3; Length 722;
Best Local Similarity 80.0%; Pred. No. 90;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCTGGAAGTGCATCCAAATTCAGGT 26
Db 625 TATGGAACAGCATCCCAATTCAGAT 649

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Job time : 54 secs

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Run on: September 1, 2004, 21:26:22 ; Search time 247 Seconds
(without alignments)
557.894 Million cell updates/sec

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Perfect score: 28
Sequence: 1 gcttgaactgcattcaattcagggttc 28
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3237270 seqs, 2460713050 residues
Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	28	100.0	28	14	US-10-028-415-2
C 3	28	100.0	28	14	US-10-028-415-11
C 4	28	100.0	2165	9	US-09-802-669-94
C 5	28	100.0	2165	13	US-10-619-220-94
C 6	28	100.0	2380	9	US-09-834-291-3
C 7	28	100.0	2827	9	US-09-834-291-4
C 8	28	100.0	3212	9	US-09-834-291-1
C 9	28	100.0	28118	13	US-10-282-174-402
C 10	28	100.0	28118	13	US-10-282-174-403
C 11	28	100.0	45121	12	US-09-997-722-10
C 12	19.2	68.6	275449	13	US-10-087-192-520
C 13	19	67.9	1608	15	US-10-311-455-2392
C 14	19	67.9	2171	13	US-10-424-599-11731

C 15	19	67.9	34562	16	US-10-417-476-28	Sequence 28, Appl
C 16	19	67.9	108359	15	US-10-191-807-3	Sequence 3, Appli
C 17	19	67.9	160771	17	US-10-450-826-86	Sequence 86, Appl
C 18	18.8	67.1	269	13	US-10-424-599-115558	Sequence 115558, A
C 19	18.6	66.4	508	10	US-09-918-995-24092	Sequence 24092, A
C 20	18.6	66.4	1597	16	US-10-108-260A-1917	Sequence 1917, Ap
C 21	18.6	66.4	3363	13	US-10-221-278-85	Sequence 85, Appl
C 22	18.6	66.4	3363	16	US-10-291-172-85	Sequence 39, Appl
C 23	18.6	66.4	3414	15	US-10-119-926-39	Sequence 20446, A
C 24	18.4	65.7	204	16	US-10-027-632-20446	Sequence 22299, A
C 25	18.4	65.7	501	10	US-09-918-995-22299	Sequence 347, App
C 26	18.4	65.7	509	9	US-09-978-295A-347	Sequence 347, App
C 27	18.4	65.7	509	9	US-09-978-697-347	Sequence 347, App
C 28	18.4	65.7	509	9	US-09-978-192A-347	Sequence 347, App
C 29	18.4	65.7	509	9	US-09-999-832A-347	Sequence 347, App
C 30	18.4	65.7	509	10	US-09-978-189-347	Sequence 347, App
C 31	18.4	65.7	509	10	US-09-978-608A-347	Sequence 347, App
C 32	18.4	65.7	509	10	US-09-978-585A-347	Sequence 347, App
C 33	18.4	65.7	509	10	US-09-978-191A-347	Sequence 347, App
C 34	18.4	65.7	509	10	US-09-978-403A-347	Sequence 347, App
C 35	18.4	65.7	509	10	US-09-978-564A-347	Sequence 347, App
C 36	18.4	65.7	509	10	US-09-999-833A-347	Sequence 347, App
C 37	18.4	65.7	509	10	US-09-981-915A-347	Sequence 347, App
C 38	18.4	65.7	509	10	US-09-978-824-347	Sequence 347, App
C 39	18.4	65.7	509	10	US-09-918-585A-347	Sequence 347, App
C 40	18.4	65.7	509	10	US-09-978-423A-347	Sequence 347, App
C 41	18.4	65.7	509	10	US-09-978-193A-347	Sequence 347, App
C 42	18.4	65.7	509	10	US-09-999-830A-347	Sequence 347, App
C 43	18.4	65.7	509	10	US-09-978-757A-347	Sequence 347, App
C 44	18.4	65.7	509	10	US-09-978-187B-347	Sequence 347, App
C 45	18.4	65.7	509	10	US-09-978-643A-347	Sequence 347, App

ALIGNMENTS

RESULT 1
US-09-997-905A-29/c
; Sequence 29, Application US/09997905A
; Publication No. US20030074684A1
; GENERAL INFORMATION:
; APPLICANT: Benitec Australia Ltd
; APPLICANT: State of Queensland through its Department of Primary Industries
; TITLE OF INVENTION: Control of Gene Expression
; FILE REFERENCE: M80219470
; CURRENT APPLICATION NUMBER: US/09/997,905A
; CURRENT FILING DATE: 2002-11-30
; PRIOR APPLICATION NUMBER: US 09/100,812
; PRIOR FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 28
; TYPE: DNA
; ORGANISM: double-stranded
US-09-997-905A-29

Query Match 100.0%; Score 28; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGAAGTGCATCCAAATTCAGGTTTC 28
Db 28 GCTTGAAGTGCATCCAAATTCAGGTTTC 1

RESULT 2
US-10-028-415-2
; Sequence 2, Application US/10028415
; Publication No. US20020151063A1
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; APPLICANT: Watson, James D.

; TITLE OF INVENTION: Methods for Modulating Apoptotic Cell

; FILE REFERENCE: 11000.1004c3

; CURRENT APPLICATION NUMBER: US/10/028.415

; CURRENT FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: PCT/NZ01/00286

; PRIOR FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: US 09/724,809

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/036,004

; PRIOR FILING DATE: 1998-03-04

; PRIOR APPLICATION NUMBER: US 08/713,557

; PRIOR FILING DATE: 1996-08-30

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 28

; TYPE: DNA

; ORGANISM: Human

US-10-028-415-2

Query Match 100.0%; Score 28; DB 14; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.0032;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 28

DB 1 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 28

RESULT 3

US-10-028-415-11/c

; Sequence 11, Application US/10028415

; Publication No. US20020151063A1

; GENERAL INFORMATION:

; APPLICANT: Lasham, Annette

; TITLE OF INVENTION: Methods for Modulating Apoptotic Cell

; FILE REFERENCE: 11000.1004c3

; CURRENT APPLICATION NUMBER: US/10/028.415

; CURRENT FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: PCT/NZ01/00286

; PRIOR FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: US 09/724,809

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/036,004

; PRIOR FILING DATE: 1998-03-04

; PRIOR APPLICATION NUMBER: US 08/713,557

; PRIOR FILING DATE: 1996-08-30

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 28

; TYPE: DNA

; ORGANISM: Human

US-10-028-415-11

Query Match 100.0%; Score 28; DB 14; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.0032;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 28

DB 28 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 1

RESULT 4

US-09-802-669-94

; Sequence 94, Application US/09802669

; Patent No. US20020004490A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Marcussen, Eric G.

; APPLICANT: Wyatt, Jacqueline

; APPLICANT: Zhang, Hong

; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

; FILE REFERENCE: ISPH-545

; CURRENT APPLICATION NUMBER: US/09/802,669

; CURRENT FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: US 09/665,615

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 09/290,640

; PRIOR FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 94

; LENGTH: 2165

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1782)...(1813)

US-09-802-669-94

Query Match 100.0%; Score 28; DB 9; Length 2165;

Best Local Similarity 100.0%; Pred. No. 0.0075;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 28

DB 747 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 774

RESULT 5

US-10-619-220-94

; Sequence 94, Application US/10619220

; Publication No. US20040033979A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Marcussen, Eric G.

; APPLICANT: Wyatt, Jacqueline

; APPLICANT: Zhang, Hong

; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

; FILE REFERENCE: ISPH-545

; CURRENT APPLICATION NUMBER: US/10/619,220

; CURRENT FILING DATE: 2003-07-14

; PRIOR APPLICATION NUMBER: 09/802,669

; PRIOR FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: US 09/665,615

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 09/290,640

; PRIOR FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 94

; LENGTH: 2165

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1782)...(1813)

US-10-619-220-94

Query Match 100.0%; Score 28; DB 13; Length 2165;

Best Local Similarity 100.0%; Pred. No. 0.0075;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 28

DB 747 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 774

RESULT 6

US-09-834-291-3

; Sequence 3, Application US/09834291


```
; Patent No. US20020042064A1
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-3

Query Match      100.0%; Score 28; DB 9; Length 2380;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
Db 746 GTCGGAAGTGCATCCAAATTCAGGTTTC 773

RESULT 7
US-09-834-291-4
; Sequence 4, Application US/09834291
; Patent No. US20020042064A1
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4

Query Match      100.0%; Score 28; DB 9; Length 2827;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
Db 1193 GTCGGAAGTGCATCCAAATTCAGGTTTC 1220

RESULT 8
US-09-834-291-1
; Sequence 1, Application US/09834291
; Patent No. US20020042064A1
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
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; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match      100.0%; Score 28; DB 9; Length 3212;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
Db 1192 GTCGGAAGTGCATCCAAATTCAGGTTTC 1219

RESULT 9
US-10-282-174-402
; Sequence 402, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelabi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 402
; LENGTH: 28118
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-174-402

Query Match      100.0%; Score 28; DB 13; Length 28118;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGGAAGTGCATCCAAATTCAGGTTTC 28
Db 1186 GTCGGAAGTGCATCCAAATTCAGGTTTC 1213
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RESULT 10
 US-10-282-174-403
 ; Sequence 403, Application US/10282174
 ; Publication No. US20030224380A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Becker, Kenneth David
 ; APPLICANT: Velicelebi, Gonul
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Wang, Xin
 ; APPLICANT: Tanzi, Rudolph E.
 ; APPLICANT: Bertram, Lars
 ; APPLICANT: Saunders, Aleister J.
 ; APPLICANT: Mullin, Kristina M.
 ; APPLICANT: Sampson, Andrew Johnson
 ; APPLICANT: Blacker, Deborah Lynne
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
 ; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
 ; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
 ; FILE REFERENCE: 37481-3308
 ; CURRENT APPLICATION NUMBER: US/10/282,174
 ; CURRENT FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: US 60/339,525
 ; PRIOR FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: US 60/338,010
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/336,929
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/338,363
 ; PRIOR FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: US 60/337,052
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: US 60/368,919
 ; PRIOR FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 403
 ; LENGTH: 28118
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 199,213,843,1530,1550,14525,14714,18982,19069,20412,20552,
 ; LOCATION: 23199,23416,24890,26359,2967,3103,5335,5345,6074,9374,9907
 ; OTHER INFORMATION: N is any
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 9936,10937,11200,11279,11359,11503,11511,11587,11694,11905,
 ; LOCATION: 12193,12208,12238,18511,18567,18982,19069,20640,21585,22439
 ; OTHER INFORMATION: N is any
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 23416,25081,26359,26878,27670
 ; OTHER INFORMATION: N is any
 ; US-10-282-174-403

Query Match 100.0%; Score 28; DB 13; Length 28118;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTGCATCCAAATTCAGGTT 28
 DB 1186 GTCTGGAAGTGCATCCAAATTCAGGTT 1213

RESULT 11
 US-09-997-722-10
 ; Sequence 10, Application US/09997722
 ; Publication No. US20040072154A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David
 ; APPLICANT: Engelhard, Eric
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: A-71171/RMS/DCF

; CURRENT APPLICATION NUMBER: US/09/997,722
 ; CURRENT FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: US 09/747,377
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 09/798,586
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 301
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 45121
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-997-722-10

Query Match 100.0%; Score 28; DB 12; Length 45121;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTGCATCCAAATTCAGGTT 28
 DB 9186 GTCTGGAAGTGCATCCAAATTCAGGTT 9213

RESULT 12
 US-10-087-192-520/C
 ; Sequence 520, Application US/10087192
 ; Publication No. US20020182586A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Engelhard, Eric K.
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: 52945200122
 ; CURRENT APPLICATION NUMBER: US/10/087,192
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 09/747,377
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 09/798,586
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 2059
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 520
 ; LENGTH: 275449
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(275449)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-087-192-520

Query Match 68.6%; Score 19.2; DB 13; Length 275449;
 Best Local Similarity 87.5%; Pred. No. 2.7e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCGAAGTGCATCCAAATTCAGGTT 27
 DB 113532 TCGAAGTGCATCCAAATTCAGGTT 113509

RESULT 13
 US-10-311-455-2392/C
 ; Sequence 2392, Application US/10311455
 ; Publication No. US20030143606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oler, Alexander
 ; APPLICANT: PIEPENBROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
 ; TITLE OF INVENTION: Cytosine methylation
 ; FILE REFERENCE: 5013.1014
 ; CURRENT APPLICATION NUMBER: US/10/311,455
 ; CURRENT FILING DATE: 2002-12-16

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; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2392
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2392

Query Match      67.9%; Score 19; DB 15; Length 1608;
Best Local Similarity 81.5%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCTGGAAGTCGATCAAAATTCAGGTC 28
Db      1175 TCTAAACTACATCAAAATTCAAATTC 1149

RESULT 14
US-10-424-599-11731/c
; Sequence 11731; Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 11731
; LENGTH: 2171
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110600C.1
US-10-424-599-11731

Query Match      67.9%; Score 19; DB 13; Length 2171;
Best Local Similarity 81.5%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCTGGAAGTCGATCAAAATTCAGGTC 28
Db      742 TCTTGAAGTCATTCATTTCAGGCTC 716

RESULT 15
US-10-417-476-28/c
; Sequence 28; Application US/10417476
; Publication No. US20040002102A1
; GENERAL INFORMATION:
; APPLICANT: Litman, Gary W
; APPLICANT: Hawke, No. US20040002102A1 A.
; APPLICANT: Yoder, Jeffrey A.
; APPLICANT: Eason, Donna D.
; TITLE OF INVENTION: BIVM (Basic, Immunoglobulin-Like Variable Motif-Containing) Gene,
; TITLE OF INVENTION: Transcriptional Products, and Uses Thereof
; FILE REFERENCE: USF-103X
; CURRENT APPLICATION NUMBER: US/10/417,476
; CURRENT FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28

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; LENGTH: 34562
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (349)..(554)
; OTHER INFORMATION: KDEL exon
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1630)..(2075)
; OTHER INFORMATION: KDEL exon
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2300)..(2681)
; OTHER INFORMATION: Exon A
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2794)..(2835)
; OTHER INFORMATION: Exon B
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3265)..(3579)
; OTHER INFORMATION: Exon C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9571)..(10171)
; OTHER INFORMATION: Exon 1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9696)..(9698)
; OTHER INFORMATION: Translation initiation codon (ATG)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10945)..(11071)
; OTHER INFORMATION: Exon 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12030)..(12125)
; OTHER INFORMATION: Exon 3
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12562)..(12666)
; OTHER INFORMATION: Exon 4
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12885)..(12979)
; OTHER INFORMATION: Exon 5
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16756)..(16962)
; OTHER INFORMATION: n = a, c, g, or t; length of "nnnnnnnnnn" nucleotides is undere
; OTHER INFORMATION: mined.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20039)..(20231)
; OTHER INFORMATION: Exon 6
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21686)..(21772)
; OTHER INFORMATION: Exon 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (24881)..(24977)
; OTHER INFORMATION: Exon 8
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25952)..(27613)
; OTHER INFORMATION: Exon 9
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26243)..(26245)
; OTHER INFORMATION: Translation termination codon (TGA)
US-10-417-476-28

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Thu Sep 2 08:32:22 2004

us-10-028-415-2.rnpb

Page 6

Query Match 67.9%; Score 19; DB 16; Length 34562;
Best Local Similarity 81.5%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGGAACATGATCCAAATTCAGTT 27
|||
Db 19650 GTCGGAATCTACATCCAACTTAAAGTT 19624

Search completed: September 1, 2004, 22:39:27
Job time : 249 secs

OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 17:35:32 ; Search time 1821 Seconds
(without alignments)
459.166 Million cell updates/sec

Title: US-10-028-415-2

Perfect score: 28

Sequence: 1 gctggaactgcatccaaattcaggttc 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_estum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.6	73.6	502	BZ194237	BZ194237 CH230-465
2	20.2	72.1	388	10 BF941188	BF941188 7d94f07.x
3	20.2	72.1	916	13 BX372157	BX372157 BX372157
4	20	71.4	464	14 CB891255	CB891255 EST648224

5 20 71.4 472 14 W24797
6 20 71.4 473 9 AR660188
7 20 71.4 523 10 BF485087
8 20 71.4 525 14 CA718977
9 20 71.4 553 10 BF081044
10 20 71.4 757 29 BX148561
11 20 71.4 845 29 CG972280
12 20 71.4 855 12 BG418680
13 20 71.4 959 13 BX370255
14 19.8 70.7 411 12 B1713285
15 19.8 70.7 530 13 BX526617
16 19.8 70.7 537 28 AZ812626
17 19.8 70.7 689 12 BG866139
18 19.8 70.7 692 12 B1647982
19 19.8 70.7 719 12 B1150689
20 19.8 70.7 779 13 BU611225
21 19.8 70.7 791 12 B1694358
22 19.8 70.7 879 12 B1557142
23 19.8 70.7 892 10 B181589
24 19.8 70.7 912 13 BQ926032
25 19.8 70.7 927 14 CF583902
26 19.6 70.0 324 13 BQ703424
27 19.6 70.0 398 14 R93603
28 19.6 70.0 460 14 CD482962
29 19.6 70.0 556 29 FR0021171
30 19.6 70.0 611 29 FR0021181
31 19.6 70.0 658 10 BF137351
32 19.2 68.6 275 10 BF560422
33 19.2 68.6 451 28 AQ684637
34 19.2 68.6 527 9 AL796563
35 19.2 68.6 594 14 CB515058
36 19.2 68.6 636 29 CQ203423
37 19.2 68.6 655 12 EG591694
38 19.2 68.6 672 14 CF440668
39 19.2 68.6 674 28 BH189737
40 19.2 68.6 674 28 CNS07TGS
41 19.2 68.6 678 28 CC310629
42 19.2 68.6 704 13 CA061797
43 19.2 68.6 725 14 CF441901
44 19.2 68.6 737 14 CF441539
45 19.2 68.6 739 14 CF438864

ALIGNMENTS

RESULT 1
BZ194237
LOCUS
DEFINITION
CH230-465F5.TJB CHORI-230 Segment 2 Rattus norvegicus genomic clone
BZ194237
BZ194237.1 GI:23852289
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 502)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat PAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other_GSSs: CH230-465F5.TVB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

BZ194237 502 bp DNA linear GSS 11-OCT-2002
CH230-465F5.TJB CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-465F5, Genomic survey sequence.

W24797 zc65f05.r1
AR660188 00028 MTR
BF485087 XHE1793 C
CA718977 Wkm2n.pk0
BF081044 233889 MA
BX148561 Danilo rer
CG972280 MBEAX48TR
BG418680 HVSMEK002
BX370255 BX370255
B1713285 ic86e02.Y
BX526617 BX526617
AZ812626 2M0079L19
BG866139 602784971
B1647982 603276055
B1150689 602915069
BU611225 UI-M-F10-
BF694358 603346927
B1557142 603239113
B181589 601808891
BQ926032 AGENCOURT
CF583902 AGENCOURT
BQ703424 EST387 al
R93603 YQ38C10.r1
CD482962 at01-7ms
AL014048 F.rubripe
BF137351 601780720
BF560422 UI-R-R1-g
AQ684637 HS 5479 B
AL796563 AL796563-
CB515058 s8alr3b50
CQ203423 tigr-g88-
EG591694 EST499536
CF440668 EST677013
BH189737 001.G.16-
AL626686 T3 end of
CC310629 TAM32-20L
CA061797 s8alr3b50
CF441901 EST678246
CF441539 EST677884
CF438864 EST675209

Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdj@chomail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 465 row: F column: 5
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers

```
1. 502
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-465F5"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SSHsd/MCW) BAC library produced by
Pieter de Jong"
```

ORIGIN

```
Query Match 73.6%; Score 20.6; DB 28; Length 502;
Best Local Similarity 85.2%; Pred. No. 4.3e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GTCTGGAAGTGCATCCAAATTCAGGTT 27
|||||
DB 379 GTCTGGAAGTGCATCCAAATTCAGGTT 405
|||||
```

RESULT 2

LOCUS

```
DEFINITION BF941188 388 bp mRNA linear EST 22-JAN-2001
IMAGE:3280668 3', mRNA sequence.
```

ACCESSION

```
BF941188
```

VERSION

```
BF941188.1 GI:12358508
```

KEYWORDS

```
EST.
```

SOURCE

```
Homo sapiens (human)
```

ORGANISM

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
1 (bases 1 to 388)
```

```
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
```

```
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
```

```
Tumor Gene Index
```

```
Unpublished (1997)
```

```
Contact: Robert Strausberg, Ph.D.
```

```
Email: cgabs-x@mail.nih.gov
```

```
Tissue Procurement: Dr. James Lupski
```

```
cDNA Library Preparation: Lupski Laboratory
```

```
DNA sequencing by: The I.M.A.G.E. Consortium (LLNL)
```

```
Clone distribution: NCI-CGAP clone distribution information can be
```

```
found through the I.M.A.G.E. Consortium/LLNL at:
```

```
infoimage.llnl.gov
```

```
Seq primer: -40UP from Gibco.
```

```
1. 388
```

```
/organism="Homo sapiens"
```

```
/mol_type="mRNA"
```

```
/db_xref="taxon:9606"
```

```
/clone="IMAGE:3280668"
```

```
/sex="male"
```

```
/tissue_type="dorsal root ganglia"
```

```
/dev_stage="adult, 36 yr"
```

```
/lab_host="DH10B"
```

```
/clone_lib="Lupski dorsal root ganglion"
```

```
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
```

```
NotI. Site 2: SalI. cDNA made by oligo-dT priming
```

ORIGIN

```
Query Match 72.1%; Score 20.2; DB 10; Length 388;
Best Local Similarity 88.0%; Pred. No. 5.8e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 TCTGGAAGTGCATCCAAATTCAGGT 26
|||||
DB 228 TCTGGAAGTGCATCCAAATTCAGT 252
|||||
```

RESULT 3

LOCUS

```
DEFINITION BX372157 916 bp mRNA linear EST 08-MAY-2003
CDNA clone CS0DK010YH06 3-PRIME, mRNA sequence.
```

ACCESSION

```
BX372157
```

VERSION

```
BX372157.1 GI:30434025
```

KEYWORDS

```
EST.
```

SOURCE

```
Homo sapiens (human)
```

ORGANISM

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
1 (bases 1 to 916)
```

```
Li,W.B., Gruber,C., Jesse,J., and Polayes,D.
```

```
Full-length cDNA libraries and normalization
```

```
Unpublished (2001)
```

```
Contact: Genoscope
```

```
Genoscope - Centre National de Sequencage
```

```
BP 191 91006 EVRY cedex - France
```

```
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
```

```
Library was constructed by Life Technologies, a division of
```

```
Invitrogen. This sequence belongs to sequence cluster 118.f For
```

```
more information about this cluster, see
```

```
http://www.genoscope.cns.fr/
```

```
cgi-bin/cluster.cgi?seq=CS0BAI040ZE02_CS03757_1acluster=118.f.
```

```
Contact : Feng Liang Email : fliang@lifetech.com URL :
```

```
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
```

```
Faraday Avenue Genoscope sequence ID : CS0BAI040ZE02_CS03757_1.
```

```
Location/Qualifiers
```

```
1. 916
```

```
/organism="Homo sapiens"
```

```
/mol_type="mRNA"
```

```
/db_xref="taxon:9606"
```

```
/clone="CS0DK010YH06"
```

```
/cell_type="HELA CELLS COT 25-NORMALIZED"
```

```
/clone_lib="HELA"
```

```
/note="1st strand cDNA was primed with a NotI-oligo(dT)"
```

```
primer. Five prime end enriched, double-strand cDNA was
```

```
digested with Not I and cloned into the Not I and EcoR V
```

```
sites of the pCMVSPORT 6 vector. Library was normalized."
```

```
18
```

```
/dev_stage="adult, 36 yr"
```

```
/lab_host="DH10B"
```

```
/clone_lib="Lupski dorsal root ganglion"
```

```
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
```

```
NotI. Site 2: SalI. cDNA made by oligo-dT priming
```

```
18
```

```
18
```

```
18
```

```
18
```

```
18
```

Directionally cloned using the following adaptors:

```
5'-TGAGCCCGGCGTCCG-3' and
5'-GACTAGTCTAGATCGGAGCGGCGGCGCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
```

ORIGIN

```
Query Match 72.1%; Score 20.2; DB 13; Length 916;
Best Local Similarity 88.0%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 4 TGGAACTGCATCCAAATTCAGGTT 28
|||||
DB 816 TGGAACTGCATCCAAATTCAGGTC 840
|||||
```

RESULT 4

LOCUS

LOCUS	CB891255	464 bp	mrna	linear	EST 24-APR-2003
DEFINITION	EST648224	KV3 Medicago truncatula	cdna clone	KV3-49L11	mrna
ACCESSION	CB891255				
VERSION	CB891255				
KEYWORDS	EST.				
SOURCE	Medicago truncatula	(barrel medic)			
ORGANISM	Medicago truncatula				
REFERENCE	1	(bases 1 to 464)			
AUTHORS	VandenBosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.				
TITLE	ESTs from roots of Medicago truncatula 72 h after Rhizobium inoculation, 2801				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: VandenBosch K Department of Plant Biology University of Minnesota 220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA Tel: 612 624 2755 Fax: 612 625 1738 Email: kvanden@ccs.umn.edu TIGR sequence name: MTEC067K More information is available at: www.medicago.org Seq primer: SKmod (CTA GAA CTA gtc gat CC).				

```

FEATURES
Location/Qualifiers
1...464
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="Genotype A17"
/db_xref="taxon:380"
/clones="KV3-45L11"
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain XLOLR"
/clone_lib="KV3"
/note="vector: pluescript SK -; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

```

ORIGIN

```
Query Match      71.4%; Score 20; DB 14; Length 464;
Best Local Similarity 82.1%; Pred. No. 7.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Caps 0;
```

Qy 1 GTCTGGAAGCTGCATCCAAATTCAGGTTCT 28
Db 135 GGCTTGCACCTGCATCCAAATACAGCTTC 162

RESULT 5	W24797	472 bp	linear	EST 11-OCT-1996
LOCUS	W24797			
DEFINITION	z665f05.x1 Soares fetal heart NbH19w Homo sapiens cDNA clone IMAGE:327201 5' . mRNA sequence.			

ACCESSION	W24797	
VERSION	W24797.1	GI:1303640
KEYWORDS	EST.	
SOURCE	Hom sapiens (human)	
ORGANISM	Hom sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 472)	
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Ho, J., Miller, M., Mullan, M., Kucaba, T., Le, M., Lennon, G., Marra, M., et al.	

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2873 Std Error: 0.00
Seq primer: mob.REGA-ET
High quality sequence stop: 311.

FEATURES
SOURCE

```

i: 172
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1261403"
/db_xref="taxon:9606"
/clone="IMAGE:327201"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicil
/clone_lib="Soares fetal
/note="Organ: heart; Vec
modified polylinker; Site
strand cDNA was primed w
TGTTACCAATCTGAATGGAGCGG
double-stranded cDNA was
adapters (Pharmacia), dig
the Not I and Eco RI site
(Pharmacia). Library wen
normalization to a Cot =
M.Fauna Bonaldo. This l
same fetus as the fetal
NHHL19W."

```

ORIGIN

Query Match	71.4%;	Score 20;
Best Local Similarity	82.1%;	Pred. No. 7
Matches	23;	Conservative 0; Mismatch

Qy 1 GTCTGGAAGTCATCCAAATTCAGGTC 28

87 GTCTAGAACTGGATTCAAATTCAGATTC 11

ORIGIN

```

Query Match      71.4%; Score 20; DB 14; Length 472;
Best Local Similarity 82.1%; Pred. No. 7.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCTGGAACATGCATCCAAATTCAGGTTTC 28
Db 87 GTCTAGAACTGGATTCATCAATTCAGATTC 114

```

9 T.111535

AA660188	AA660188	473 bp	mRNA	linear	EST 08-MAR-2000
LOCUS	00028 MURHE	truncatula	cdna 5'	similar to receptor-like	
DEFINITION	protein kinase, mRNA sequence.				
ACCESSION	AA660188				
VERSION	AA660188.1	GI:2604232			
KEYWORDS	EST				
SOURCE	Medicago truncatula (barrel medic)				
ORGANISM	Medicago truncatula				
REFERENCE	1 (bases 1 to 473)				
AUTHORS	Covitz, P.A., Smith, L.S. and Long, S.R.				
TITLE	Expressed sequence tags from a root-hair-enriched medicago truncatula cdna library				
JOURNAL	Plant Physiol. 117 (4), 1325-1332 (1998)				
COMMENT	Contact: Long SR				
	Department of Biological Sciences and Howard Hughes Medical Institute				
	Stanford University				

Gilbert Biology, Stanford, CA 94305-5020, USA
 Tel: 650 723 3232
 Fax: 650 725 8309
 Email: fa.srl@forsythe.stanford.edu
 Seq primer: 13.

FEATURES

source

Location/Qualifiers
 1..473
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /cultivar="Jemalong"
 /db_xref="taxon:3880"
 /tissue_type="Root hairs & tips"
 /dev_stage="2-3 day old seedlings"
 /clone_lib="McRHF"
 /note="Organ: Root; Vector: pBK-CMV; Site 1: EcoRI;
 Site 2: XhoI; cDNA was synthesized from a pooled mRNA prep
 from elongating root hairs (30% w/w) and 2-3cm root tips
 (70% w/w). XhoI-oligo-dT linker-primer and EcoRI
 adaptors were used. cDNAs were cloned unidirectionally
 into lambda ZAP Express (Stratagene), amplified, and
 mass-excised into pBK-CMV vector plasmids. More
 information is available at <http://bio-srls.stanford.edu>."

ORIGIN

Query Match 71.4%; Score 20; DB 9; Length 473;
 Best Local Similarity 82.1%; Pred. No. 7.4e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28

Db 138 GGCTTGCACTGCATCCAAATACAGCTTC 165

RESULT 7

BF485087

LOCUS

DEFINITION WHE1793_C05_F092S Wheat pre-anthesis spike cDNA library Triticum
 aestivum cDNA clone WHE1793_C05_F09, mRNA sequence.

ACCESSION

BF485087

VERSION

BF485087.1

KEYWORDS

EST.

SOURCE

Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE

1 (bases 1 to 523)

AUTHORS

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
 Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L. and Tong, J.C.

TITLE

The structure and function of the expressed portion of the wheat
 genomes - Pre-anthesis spike cDNA library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: onders@nwp.usda.govSequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1..523

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHE1793_C05_F09"

/tissue_type="Spike before anthesis"

/dev_stage="Adult plant"

/lab_host="E. coli SOLR"

/clone_lib="Wheat pre-anthesis spike cDNA library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
 greenhouse. Whole spike with awns trimmed, white, green
 and yellow anther were collected and total RNA, and
 poly(A) RNA were prepared, a cDNA library was made, and
 the cDNA clones were in vivo excised to give pBluescript
 phagemids in the TV Close lab (Choi, Close, Fenton) at
 the University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

ORIGIN

Query Match 71.4%; Score 20; DB 10; Length 523;
 Best Local Similarity 82.1%; Pred. No. 7.7e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28

Db 83 GACTGGAACTGCTCCATAATCAGGTTTC 110

RESULT 8

CA718977

LOCUS

DEFINITION

wkm2n.pk002.06 wkm2n Triticum aestivum cDNA clone wkm2n.pk002.06 5'

end, mRNA sequence.

ACCESSION

CA718977

VERSION

CA718977.1

KEYWORDS

EST.

SOURCE

Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE

1 (bases 1 to 525)

AUTHORS

Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.

TITLE

DuPont Wheat cDNA Sequence

JOURNAL

Unpublished (2002)

COMMENT

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: M13.

Location/Qualifiers

1..525

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Spring wheat"

/db_xref="taxon:4565"

/clone="wkm2n.pk002.06"

/tissue_type="kernel"

/lab_host="DH108"

/clone_lib="wkm2n"

/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
 XhoI; Wheat (Triticum aestivum L.) kernel malted 175 hours
 at 4 C, normalized"

ORIGIN

Query Match 71.4%; Score 20; DB 14; Length 525;
 Best Local Similarity 82.1%; Pred. No. 7.7e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCTGGAACTGCATCCAAATTCAGGTTTC 28

Db 407 GTCTTGAACAGCATCCAGCTTAGGTTTC 434

RESULT 9

BF081044/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

BF081044
233889 MARCH 2PTG Sus scrofa cDNA 5', mRNA sequence.
BF081044
BF081044.1 GI:10874874
EST.
Sus scrofa (pig)
Sus scrofa
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 553)
Fahrenkrug, S.C., Smith, T.P.L., Preking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,
Quackenbush, J., and Keefe, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGAG
Plate: 54 row: P column: 4
Seq primer: ATTAGTGACATATAG.
Location/Qualifiers
1..553
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/issue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARCH 2PTG"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

Query Match 71.4%; Score 20; DB 10; Length 553;
Best Local Similarity 82.1%; Pred. No. 7.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCCTGGAACCTCATCAAAATTCAGGTTTC 28
DB 392 GTGTGGAACCTCATCAAAATTCAGGTTTC 365

RESULT 10
BX148561/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

BX148561
Danio rerio genomic clone DKEY-101C6, genomic survey sequence.
BX148561
BX148561.1 GI:27979989
GSS.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 757)
Humphray, S.J., Huckle, E., and Durham, J.L.
Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 101C6. 101C6 is
part of the Daniokey BAC Library created by R. Piasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
source
1..757
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-101C6"
/tissue_type="Testis"
/note="Vector pIndigoBAC-536"

ORIGIN
Query Match 71.4%; Score 20; DB 29; Length 757;
Best Local Similarity 82.1%; Pred. No. 8.5e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCCTGGAACCTCATCAAAATTCAGGTTTC 28
DB 347 GTCCGGAACCTCATCAAAATTCAGGTTTC 320

RESULT 11
CG972280
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CG972280
MBEAX48TR mth2 Medicago truncatula genomic clone 16H24, genomic
survey sequence.
CG972280
CG972280.1 GI:39898059
GSS.
Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 845)
Town, C.D., Shetty, J., Koo, H., and Feldblyum, T.F.
Sequencing of BAC ends from Medicago truncatula
Unpublished (2003)
Other GSSs: MBEAX48TFB
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seq primer: CAGGAACAGCTATGAC
Class: BAC ends.
Location/Qualifiers
1..845
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="16H24"
/note="Vector: pBelobAC11; Site 1: HindIII; Site 2:
HindIII; Cook, D.R. and Kim, D.J., unpublished"

ORIGIN
Query Match 71.4%; Score 20; DB 29; Length 845;
Best Local Similarity 82.1%; Pred. No. 8.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCCTGGAACCTCATCAAAATTCAGGTTTC 28
DB 313 GGCTTGCACTGCATCAAAATTCAGGTTTC 340

RESULT 12
BG418680/c

LOCUS	855 bp	linear	EST 23-OCT-2001
DEFINITION	HY5MEK023008f Hordeum vulgare testa/pericarp EST library		
	HYCDNA0013 (normal) Hordeum vulgare subsp. vulgare cDNA clone		
	HY5MEK023008f, mRNA sequence.		
ACCESSION	BG4119680		
VERSION	BG4119680.2		
KEYWORDS	GI:16333779		
SOURCE	EST		
ORGANISM	Hordeum vulgare subsp. vulgare		
	Hordeum vulgare subsp. vulgare		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
	Poideae; Triticeae; Hordeum.		
REFERENCE	1 (bases 1 to 855)		
AUTHORS	Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Kannangara,G., von		
	Wetstein,D., Akhunov,E., Chin,A., Choi,D.W., Fenton,R.D.,		
	Kianian,P., Otto,C., Simons,K., Zhang,D., Begum,D., Frisch,D.,		
	Yu,Y., Henry,D., Falmer,M., Rambo,T., Simmons,J., Oates,R. and		
	Main,D.		
TITLE	Development of a genetically and physically anchored EST resource		
JOURNAL	for barley genomics: Morex testa/pericarp cDNA library		
COMMENT	Unpublished (2001)		
	On Mar 13, 2001 this sequence version replaced gi:13324231.		
	Contact: Wing RA		
	Clemson University Genomics Institute		
	Clemson University		
	100 Jordan Hall, Clemson, SC 29634, USA		
	Tel: 864 656 7288		
	Fax: 864 656 4293		
	Email: twing@clemson.edu		
	Total hg bases = 507		
	Seq primer: AATTAACCTCACTAAAGGG		
FEATURES	High quality sequence stop: 568.		
	Location/Qualifiers		

1. 855

Source

/organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Morex"
 /sub_species="vulgate"
 /db_xref="taxon:112509"
 /clone="HVSMEK0023008f"
 /tissue_type="testa/pericarp"
 /lab_host="TJUC121"
 /clone_lib="Hordeum vulgare testa/pericarp EST library HVCNDA0013 (normal)"
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 Plants were raised from seeds in a Controlled Environment growth chamber maintained in continuous light at 18°C, and testa and pericarp were dissected from developing kernels at Washington State University, Pullman, WA (Kannangara, von Weststein). Total RNA was prepared, poly(A) RNA was purified, one cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley Genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

71.4%; Score 20; DB 12; Length 855;
 Best Local Similarity 82.1%; Pred. No. 8.8e+02;

ORIGIN

Query Match 71.4%; Score 20; DB 13; Length 959;
 Best Local Similarity 82.1%; Pred. No. 9.1e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCTGGAACGTGCATCCAAATTCAGGTTTC 28
 Db 715 GGCTGGAACGTGCTCCCACTTGAGGTTTC 688

RESULT 14
 BI713285
 LOCUS BI713285 411 bp mRNA linear EST 12-MAR-2002
 DEFINITION ic86602.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MWS1 Mus
 musculus cDNA clone IMAGE:5660619 5', mRNA sequence.
 ACCESSION BI713285
 VERSION BI713285.1 GI:156888980
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 411)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Breselli,J., Gradwohl,G., Clifton,S.

Query Match 71.4%; Score 20; DB 12; Length 855;
 Best Local Similarity 82.1%; Pred. No. 8.8e+02;

ORIGIN

Query Match 71.4%; Score 20; DB 13; Length 959;
 Best Local Similarity 82.1%; Pred. No. 9.1e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCTGGAACGTGCATCCAAATTCAGGTTTC 28
 Db 715 GGCTGGAACGTGCTCCCACTTGAGGTTTC 688

RESULT 14
 BI713285
 LOCUS BI713285 411 bp mRNA linear EST 12-MAR-2002
 DEFINITION ic86602.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MWS1 Mus
 musculus cDNA clone IMAGE:5660619 5', mRNA sequence.
 ACCESSION BI713285
 VERSION BI713285.1 GI:156888980
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 411)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Breselli,J., Gradwohl,G., Clifton,S.

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OM nucleic - nucleic search, using sw model
Run on: September 1, 2004, 19:43:07 ; Search time 1400 Seconds
(without alignments)
866.861 Million cell updates/sec

Title: US-10-028-415-2
Perfect score: 28
Sequence: 1 gcttggaactgcattccaaattcaggttc 28

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
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17: em_hum:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	100.0	28	6	AR071972	AR071972 Sequence
2	28	100.0	28	6	AR071984	AR071984 Sequence
3	28	100.0	50	6	AR072005	AR072005 Sequence
4	28	100.0	1608	9	HSFASX1	X82279 H.sapiens F
5	28	100.0	1877	9	HSAPT1	X81335 H.sapiens A
6	28	100.0	2165	9	AR432294	AR432294 Sequence
7	28	100.0	2165	9	HUMFAS	D31968 Homo sapien
8	28	100.0	2344	9	HSCD955FR	X87625 H.sapiens C
9	28	100.0	2380	6	BD237717	BD237717 p53 bindi
10	28	100.0	2380	6	AX026091	AX026091 Sequence
11	28	100.0	2827	6	BD237718	BD237718 p53 bindi
12	28	100.0	2827	6	AX026092	AX026092 Sequence
13	28	100.0	3212	6	BD237715	BD237715 p53 bindi
14	28	100.0	3212	6	AX026089	AX026089 Sequence
15	28	100.0	28339	9	AY450925	AY450925 Homo sapi
16	28	100.0	45121	6	AX695635	AX695635 Sequence
17	28	100.0	187313	9	AL157394	AL157394 Human DNA
18	21.6	77.1	197772	2	AC145295	AC145295 Pongo pyg
19	21.6	77.1	205616	2	AC146844	AC146844 Pongo pyg
20	21.2	75.7	4569	5	XLM181	Y08295 X.laevis MR
21	21.2	75.7	121355	9	AL358943	AL358943 Human DNA
22	21.2	75.7	173386	2	AL353776	AL353776 Homo sapi
23	20.8	74.3	75820	2	AC101006	AC101006 Mus muscu
24	20.8	74.3	100000	9	AP000069	AP000069 Homo sapi
25	20.8	74.3	100364	9	AC007590	AC007590 Homo sapi
26	20.8	74.3	160190	2	AC119202	AC119202 Mus muscu
27	20.8	74.3	165610	2	AC134527	AC134527 Mus muscu
28	20.8	74.3	205831	2	AC074192	AC074192 Homo sapi
29	20.8	74.3	208852	9	AC091182	AC091182 Homo sapi
30	20.8	74.3	208375	2	AC130246	AC130246 Rattus no
31	20.8	74.3	211750	9	AP006306	AP006306 Homo sapi
32	20.8	74.3	230563	2	AC094600	AC094600 Rattus no
33	20.6	73.6	280325	2	AC112293	AC112293 Rattus no
34	20.6	73.6	323304	2	AC108248	AC108248 Rattus no
35	20.2	72.1	158830	2	AC027693	AC027693 Homo sapi
36	20.2	72.1	177187	2	AC096848	AC096848 Papio anu
37	20.2	72.1	187321	2	AC092510	AC092510 Papio anu
38	20.2	72.1	210623	2	AC113027	AC113027 Mus muscu
39	20	71.4	8193	6	AX537570	AX537570 Sequence
40	20	71.4	8193	6	AX537571	AX537571 Sequence
41	20	71.4	16253	9	AY135329	AY135329 Homo sapi
42	20	71.4	126779	9	AL603882	AL603882 Human DNA
43	20	71.4	129779	9	AL359457	AL359457 Human DNA
44	20	71.4	142000	2	BX664725	BX664725 Homo sapi
45	20	71.4	145937	2	AL355600	AL355600 Homo sapi

ALIGNMENTS

RESULT 1	AR071972	Sequence 2 from patent US 5912168.	28 bp	DNA	linear	PAT 18-FEB-2000
LOCUS	AR071972	Sequence 2 from patent US 5912168.				
DEFINITION	AR071972	Sequence 2 from patent US 5912168.				
ACCESSION	AR071972	Sequence 2 from patent US 5912168.				
VERSION	AR071972.1	GI:7222860				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 28)					
AUTHORS	Watson,J.D. and Rudert,F.					
TITLE	CD95 regulatory gene sequences					
JOURNAL	Patent: US 5912168-A 2 15-JUN-1999;					
FEATURES	Location/Qualifiers					

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Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGTGGAAGTGCATCCAAATTCAGGTTTC 28
Db 1 GTCGTGGAAGTGCATCCAAATTCAGGTTTC 28

RESULT 2
AR071984/c
LOCUS          AR071984          28 bp          DNA          linear          PAT 18-FEB-2000
DEFINITION     Sequence 14 from patent US 5912168.
ACCESSION      AR071984
VERSION        AR071984.1 GI:7222872
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Watson,J.D. and Rudert,F.
TITLE          CD95 regulatory gene sequences
JOURNAL        Patent: US 5912168-A 14 15-JUN-1999;
FEATURES       Location/Qualifiers
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Query Match      100.0%; Score 28; DB 6; Length 28;
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGTGGAAGTGCATCCAAATTCAGGTTTC 28
Db 28 GTCGTGGAAGTGCATCCAAATTCAGGTTTC 1

RESULT 3
AR072005
LOCUS          AR072005          50 bp          DNA          linear          PAT 18-FEB-2000
DEFINITION     Sequence 35 from patent US 5912168.
ACCESSION      AR072005
VERSION        AR072005.1 GI:7222893
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 50)
AUTHORS        Watson,J.D. and Rudert,F.
TITLE          CD95 regulatory gene sequences
JOURNAL        Patent: US 5912168-A 35 15-JUN-1999;
FEATURES       Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTCGTGGAAGTGCATCCAAATTCAGGTTTC 28

RESULT 4
HSPASX1
LOCUS          H.sapiens Fas, Apo-1 gene (promoter and exon 1).
DEFINITION     H.sapiens Fas, Apo-1 gene (promoter and exon 1).
ACCESSION      X82279
VERSION        X82279.1 GI:673405
KEYWORDS       APO-1 gene; Fas gene.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Cheng,J., Liu,C., Koopman,W.J. and Mountz,J.D.
TITLE          Characterization of human Fas gene. Exon/intron organization and
promoter region
JOURNAL        J. Immunol. 154 (3), 1239-1245 (1995)
MEDLINE        95123075
PUBMED        7529798
REFERENCE      2 (bases 1 to 1608)
AUTHORS        Cheng,J.
TITLE          Direct Submission
JOURNAL        Submitted (20-OCT-1994) J. Cheng, Univ.of Alabama at Birmingham,
Univ. of Alabama, 701 South 19th Street, UAB Station, LHRB 473,
Birmingham, AL 35294-0007, USA
COMMENT        Related sequences: M67454 and X63717.
FEATURES       Location/Qualifiers
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/mol_type="genomic DNA"
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/map="10q23 or 10q24.1"
/tissue_type="placenta"
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1075. .1496
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gene
exon

ORIGIN
Query Match      100.0%; Score 28; DB 9; Length 1608;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGTGGAAGTGCATCCAAATTCAGGTTTC 28
Db 433 GTCGTGGAAGTGCATCCAAATTCAGGTTTC 460

RESULT 5
HSAPT1
LOCUS          H.sapiens APT gene, exon 1.
DEFINITION     H.sapiens APT gene, exon 1.
ACCESSION      X81335
VERSION        X81335.1 GI:537410
KEYWORDS       APO-1 gene; apt gene.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Behrmann,I., Walczak,H. and Krammer,P.H.
TITLE          Structure of the human APO-1 gene
JOURNAL        Eur. J. Immunol. 24 (12), 3057-3062 (1994)
MEDLINE        95104292
PUBMED        7528667
REFERENCE      2 (bases 1 to 1877)
AUTHORS        Krammer,P.H.
TITLE          Direct Submission
JOURNAL        Submitted (03-SEP-1994) P.H. Krammer, German Cancer Research
Center, Tumorimmunology Programm, Im Neuenheimer Feld 280, 69120
Heidelberg, FRG
FEATURES       Location/Qualifiers
source         1. .1877
/organism="Homo sapiens"

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 Db 745 GTCTGGAAGTCATCCAAATTCAGGTTTC 773
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RESULT 6
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 DEFINITION Sequence 94 from patent US 6653133.
 ACCESSION AR432294
 VERSION AR432294.1 GI:40194567
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 2165)
 AUTHORS Dean,N.M., Marcussen,E.G. and Wyatt,J.
 TITLE Antisense modulation of Fas mediated signaling
 JOURNAL Patent: US 6653133-A 94 25-NOV-2003;
 FEATURES Location/Qualifiers
 source 1. .2165
 /organism="unknown"
 /mol_type="genomic DNA"

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 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGAAGTCATCCAAATTCAGGTTTC 28
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 Db 747 GTCTGGAAGTCATCCAAATTCAGGTTTC 774
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RESULT 7
 HUMFAS
 LOCUS 2165 bp DNA linear PRI 07-FEB-2003
 DEFINITION Homo sapiens gene for Fas antigen, partial cds and promoter region.
 ACCESSION D31968
 VERSION D31968.1 GI:961455
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2165)
 AUTHORS Wada,N., Matsumura,M., Ohba,Y., Kobayashi,N., Takizawa,T. and Nakanishi,Y.
 TITLE Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection
 JOURNAL J. Biol. Chem. 270 (30), 18007-18012 (1995)
 MEDLINE 95355401
 PUBMED 7543095

REFERENCE 2 (bases 1 to 2165)
 AUTHORS Nakanishi,Y.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@bs.p.kanazawa-u.ac.jp, Tel:81-76-234-4424, Fax:81-76-234-4480)

FEATURES Location/Qualifiers
 source 1. .2165

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276..284
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481..489
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772..780
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934..940
/bound_moiety="AP-1"
948..955
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1436..1813
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1436..1781
1782..1813
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/translation="MLGIWTLPLV"
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 747 GTCTGGAAGTCATCCAAATTCAGGTTTC 774

RESULT 8
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DEFINITION H.sapiens CD95 gene 5' flanking region.
ACCESSION X87625
VERSION X87625.1 GI:902311
KEYWORDS beta interferon; CD95 gene; silencer.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Rudert,F., Visser,E., Forbes,L., Lindridge,E., Wang,Y. and
Watson,J.
TITLE Identification of a silencer, enhancer, and basal promoter region
JOURNAL DNA Cell Biol. 14 (11), 931-937 (1995)
MEDLINE 96069539
PUBMED 7576179
REFERENCE 2 (bases 1 to 2344)
AUTHORS Rudert,F.H.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1995) F.H. Rudert, Genesis Research &
Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
COMMENT Overlaps with X81335, & X82279-X82286.
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/map="q24.1"

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717..801
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1338..1919
1920..2344
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Db 1310 GTCTGGAAGTCATCCAAATTCAGGTTTC 1337

RESULT 9
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DEFINITION p53 binding region.
ACCESSION BD237717
VERSION BD237717.1 GI:33047487
KEYWORDS JP 2002527108-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Krammer,P., Schilling,M.M. and Oren,M.
TITLE p53 binding region
JOURNAL Patent: JP 2002527108-A 3 27-AUG-2002;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS
COMMENT CS Homo sapiens (human)
PN JP 2002527108-A/3
PD 27-AUG-2002
PP 18-OCT-1999 JP 2000577293
PR 16-OCT-1998 DE 198 47 779.1
PI PETER KRAMMER,MARTINA MUELLER SCHILLING,MOSHE OREN PC
C12N15/09,C12Q1/66,C12Q1/68,G01N33/566,C12N15/00 CC p53 binding
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/mol_type="genomic DNA"
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCTGGAAGTCATCCAAATTCAGGTTTC 28
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Db 746 GTCTGGAAGTCATCCAAATTCAGGTTTC 773

RESULT 10
AX026091
LOCUS AX026091 2380 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 3 from Patent DE19847779.
ACCESSION AX026091
VERSION AX026091.1 GI:10187522
KEYWORDS Homo sapiens (human)
SOURCE

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 3 03-FEB-2000;
JOURNAL DEUTSCHES KREBSFORSCH (DE)
FEATURES
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 746 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 773
RESULT 11
BD237718 2827 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION p53 binding region.
ACCESSION BD237718
VERSION BD237718.1 GI:33047488
KEYWORDS JP 2002527108-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2827)
Krammer, P., Schilling, M.M. and Oren, M.
p53 binding region
Patent: JP 2002527108-A 4 27-AUG-2002;
JOURNAL DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS
COMMENT OS Homo sapiens (human)
PN JP 2002527108-A/4
PD 27-AUG-2002
PF 18-OCT-1999 JP 2000577293
PI 16-OCT-1998 DE 198 47 779.1
PI PETER KRAMMER, MARTINA MUELLER SCHILLING, MOSHE OREN PC
C12N15/09, C12Q1/66, C12Q1/68, G01N33/566, C12N15/00 CC p53 binding
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FH Key Location/Qualifiers
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Db 1193 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 1220
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AX026092 2827 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION Sequence 4 from Patent DE19847779.
ACCESSION AX026092

VERSION AX026092.1 GI:10187523
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 4 03-FEB-2000;
JOURNAL DEUTSCHES KREBSFORSCH (DE)
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1193 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 1220
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BD237715 3212 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION p53 binding region.
ACCESSION BD237715
VERSION BD237715.1 GI:33047485
KEYWORDS JP 2002527108-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3212)
Krammer, P., Schilling, M.M. and Oren, M.
p53 binding region
Patent: JP 2002527108-A 1 27-AUG-2002;
JOURNAL DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS
COMMENT OS Homo sapiens (human)
PN JP 2002527108-A/1
PD 27-AUG-2002
PF 18-OCT-1999 JP 2000577293
PF 16-OCT-1998 DE 198 47 779.1
PI PETER KRAMMER, MARTINA MUELLER SCHILLING, MOSHE OREN PC
C12N15/09, C12Q1/66, C12Q1/68, G01N33/566, C12N15/00 CC p53 binding
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 28
Db 1192 GTCGTGGAACCTGCATCCAAATTCAGGTTTC 1219
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6951 /gene="TNFRSF6"
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OM protein - protein search, using sw model

Run on: August 25, 2004, 00:06:29 ; Search time 123 Seconds
(without alignments)
744.271 Million cell updates/sec

Title: US-10-028-415-40
Perfect score: 1747
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Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1747	100.0	324	6 ABO53035	Human put
3	1747	100.0	369	2 ARL14848	Protein a
4	1747	100.0	369	2 AAW00089	RAS-relat
5	1747	100.0	369	2 AAY49814	Human gli
6	1747	100.0	369	3 AAB20625	pATG29 hu
7	1743	99.8	384	6 AAO16411	Human nuc
8	1707	97.7	322	2 AAW12827	Rat TSEP-
9	1707	97.7	322	7 ABB80304	Rat Y-box
10	1707	97.7	322	7 ADE61260	Rat Prote
11	1707	97.7	322	7 ADD48835	Rat Prote
12	1707	97.7	322	5 ADE61263	Rat Prote
13	1701	97.4	322	5 ABB57039	Mouse isc
14	1701	97.4	322	7 ABB80303	Mouse Y-D
15	1699	97.3	322	7 ABB80299	Rat Y-box
16	1699	97.3	322	7 ABB80300	Rat Y-box
17	1699	97.3	322	7 ABB80297	Rat B-TEP
18	1699	96.7	322	7 ABB80302	Mouse Y-b
19	1688	96.6	322	7 ABB80305	Rat Y-box
20	1687	96.6	317	5 AAG70989	Human YB-
21	1687	96.6	317	5 AAU79748	Human DNA
22	1687	96.6	317	7 ABB80298	Human Y-b
23	1687	96.6	318	7 ADD48837	Human Pro
24	1630	93.3	302	4 AAB29744	Human Y-b
25	1534	87.8	290	6 AAE37023	Human nuc

26	1489.5	85.3	375	4 ABG18816	Novel hum
27	865.5	49.5	361	7 ADE56070	Rat Prote
28	840	48.1	372	4 AAU27828	Human ful
29	840	48.1	372	6 ABO53070	Human put
30	840	48.1	442	4 AAC06882	Human pol
31	753.5	43.1	303	4 AAU27829	Dog full-
32	739	42.3	142	4 ABG18815	Novel hum
33	731	41.8	272	3 AAB57119	Human pro
34	657.5	37.6	445	2 AAR14163	Cellular
35	543	31.1	397	4 ABG08725	Novel hum
36	502.5	28.8	121	4 ABG11756	Novel hum
37	500	28.6	315	4 ABB61702	Drosophil
38	497.5	28.5	143	4 ABG11757	Novel hum
39	495	28.3	303	4 AAU18157	Novel hum
40	495	28.3	303	5 ABG92578	Human DNA
41	495	28.3	303	7 ADC25295	Human ext
42	476.5	27.3	253	4 AAM95499	Human rep
43	476.5	27.3	253	4 ABB96182	Human tes
44	476.5	27.3	253	4 AAU18236	Novel hum
45	476.5	27.3	253	5 ABG92657	Human DNA

ALIGNMENTS

RESULT 1

AAU99516
ID AAU99516 standard; protein; 324 AA.
XX AC AAU99516;
XX DT 07-OCT-2002 (first entry)
XX DE Human YB-1 protein.
XX KW Human; apoptotic cell death; proteinaceous transcription factor;
KW regulation of gene transcription; apoptosis; p53; CD95; TRA;
KW transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;
KW tumour cell; embryonic cell; nervous system; intracellular pathogen;
KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;
KW immune system dysfunction; anti-tumour; cytostatic.
XX OS Homo sapiens.
XX PN WO200244363-A1.
XX PD 06-JUN-2002.
XX PF 28-NOV-2001; 2001WO-NZ000287.
XX PR 28-NOV-2000; 2000US-00724809.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Lasham A, Watson JD;
XX WPI; 2002-557540/59.
XX Modulating p53-mediated apoptotic cell death in a population of cells, by
modulating the amount of a transcriptional regulator of apoptosis
available to bind to a target polynucleotide in the cells.
XX Claim 3; Page 59; 62pp; English.
XX The present invention relates to methods for modulating apoptotic cell
death using proteinaceous transcription factors that regulate the
transcription of genes encoding proteins involved in apoptosis (e.g. CD95
and p53). The methods involve modulating the amount of a transcriptional
regulator of apoptosis (TRA) available to bind to a target polynucleotide
in the cells, where TRA is a member of the Y-box nucleic acid binding
CC family of polypeptides (e.g. YB-1). The methods of the invention are
useful for modulating apoptotic cell death in a population of cells,
where the cells are selected from tumour cells, cells of the immune

AC AAR14848;
XX 25-MAR-2003 (revised)
DT 30-JAN-1992 (first entry)
XX
DE Protein associated with biochemical pathway involving cAMP.
XX
XX RAS; oncogene; cancer; cyclic nucleotide phosphodiesterase.
XX
XX Homo sapiens.
XX
XX W09116457-A.
XX
XX 31-OCT-1991. 90US-00511715.
XX
XX 20-APR-1990; 90US-00511715.
XX
XX 20-APR-1990; 90US-00511715.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX Wigler MH, Colicelli JJ;
XX
XX WPI; 1991-339841/46.
XX N-PSDB; AAQ14635.
XX
XX Complementary screening for genes and prods. - e.g. RAS protein and cAMP,
XX that modify, complement or suppress genetic defect and correct associated
XX phenotypic alteration.
XX
XX Disclosure; Page 114; 169pp; English.
XX
XX In the specification this sequence is given the SEQ ID NO. 31. In the
XX text, SEQ ID NO.31 is described as the nucleotide sequence of the cDNA
XX insert from plasmid pATG29 which was able to complement a mutation in the
XX ras1 gene ! (Updated on 25-MAR-2003 to correct PA field.)
XX
XX
SQ Sequence 369 AA;
Query Match 100.0%; Score 1747; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.3e-134;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSEAEQCPAAPPAALSAADTKPCTTGSAGSGGPGGLTSAAPAGDKKVIATKVL 60
Db 46 MSSEAEQCPAAPPAALSAADTKPCTTGSAGSGGPGGLTSAAPAGDKKVIATKVL 105
QY 61 GTVKWFNVRNGYGFNRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 120
Db 106 GTVKWFNVRNGYGFNRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 165
QY 121 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSESAPEG 180
Db 166 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSESAPEG 225
QY 181 QAQQRPRRRPPPPYMRPYPGRPOYSNPPVQGEVWEGADNQAGEQGRPVQNNYRG 240
Db 226 QAQQRPRRRPPPPYMRPYPGRPOYSNPPVQGEVWEGADNQAGEQGRPVQNNYRG 285
QY 241 YRPRFRGPRQRORFREDNEEDKENQDGTQGGQPPQRRYRNFYRRRRPNPKPDG 300
Db 286 YRPRFRGPRQRORFREDNEEDKENQDGTQGGQPPQRRYRNFYRRRRPNPKPDG 345
QY 301 KETKAADPPPAENSSAPEAEOGGAE 324
Db 346 KETKAADPPPAENSSAPEAEOGGAE 369
RESULT 4
AAW00089
ID AAW00089 standard; protein; 369 AA.
XX
AC AAW00089;

XX 25-MAR-2003 (revised)
DT 09-OCT-1996 (first entry)
XX
DE RAS-related protein encoded by plasmid pATG29 (ATCC 68591).
XX
XX Human; glioblastoma; complementation; S. cerevisiae; S. pombe; Clone S46;
KW strain RS60.15B; RAS2; RAS2(vall19ala15); Xenopus laevis;
KW S6 protein kinase; Plasmid pML5; strain SKN37; CAP; adenyllyl cyclase;
KW diploid; strain SP565; ras1; ras1::LEU2; mutation.
XX
XX Homo sapiens.
XX
XX US5527896-A.
XX
XX 18-JUN-1996.
XX
XX 19-APR-1991; 91US-006888352.
XX
XX 20-APR-1990; 90US-00511715.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX Colicelli JJ, Wigler MH;
XX
XX WPI; 1996-299902/30.
XX N-PSDB; AAT34371.
XX
XX DNA mols. isolated from human glioblastoma cells - encode RAS-related or
XX cyclic nucleotide phosphodiesterase proteins.
XX
XX Claim 1; Col 107-112; 101pp; English.
XX
XX The sequences given in AAW00087-89 and AAW00101 are encoded by plasmid
XX fragments which contain human glioblastoma cell cDNA inserts which do not
XX encode phosphodiesterases. The cDNA's were obtained by complementation of
XX two genetically altered S. cerevisiae and S. pombe strains. Clone S46 was
XX selected by complementation in S. cerevisiae strain RS60.15B. This strain
XX contains a mutant allele of RAS2, RAS2(vall19ala15), which renders cells
XX unable to grow at 36 deg. C, because such cells are defective in RAS
XX function at elevated temperatures. Human cDNA's from a human glioblastoma
XX cell library were selected that could complement this defect. The deduced
XX sequence of S46 is homologous to a Xenopus laevis gene that encodes a
XX known protein kinase, the S6 protein kinase. Plasmid pML5 was selected by
XX complementation in S. cerevisiae strain SKN37. This strain contains a
XX disrupted allele of CAP, cap::HIS3. CAP encodes an adenyllyl cyclase
XX associated protein of undetermined function. As a consequence of this
XX gene disruption, SKN37 fails to grow in medium rich in amino acids. Human
XX cDNA's were chosen which could complement this defect. Plasmids pATG16
XX and pATG29 were selected by complementation in the S. pombe diploid
XX strain SP565. This strain is homozygous for disruptions of ras1
XX (ras1::LEU2). As a result of this mutation, this strain fails to
XX sporulate, and human cDNA's were selected which could complement this
XX defect. These genes have unknown function. (Updated on 25-MAR-2003 to
XX correct PF field.)
XX
XX Sequence 369 AA;
SQ
Query Match 100.0%; Score 1747; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.3e-134;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSEAEQCPAAPPAALSAADTKPCTTGSAGSGGPGGLTSAAPAGDKKVIATKVL 60
Db 46 MSSEAEQCPAAPPAALSAADTKPCTTGSAGSGGPGGLTSAAPAGDKKVIATKVL 105
QY 61 GTVKWFNVRNGYGFNRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 120
Db 106 GTVKWFNVRNGYGFNRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 165
QY 121 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSESAPEG 180
Db 166 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSESAPEG 225
XX

QY 181 QAOQRPPYRRRPPYRRPGRPOYSNPPVQGVMEGADNCGAGEQGRPVRRQNNYRG 240
 |||||
 DB 226 QAOQRPPYRRRPPYRRPGRPOYSNPPVQGVMEGADNCGAGEQGRPVRRQNNYRG 285
 |||||
 QY 241 YRPRFRGPPRQROPREDGNEEDKENQDGTQGGQPPORRYRRNFYRRRRPENPKPDG 300
 |||||
 DB 286 YRPRFRGPPRQROPREDGNEEDKENQDGTQGGQPPORRYRRNFYRRRRPENPKPDG 345
 |||||
 QY 301 KETKAADPPAENSAPAEQGGAE 324
 |||||
 DB 346 KETKAADPPAENSAPAEQGGAE 369
 |||||
 RESULT 5
 AAY49814
 ID AAY49814 standard; protein; 369 AA.
 XX
 AC AAY49814;
 XX
 XX 19-JAN-2000 (first entry)
 DT
 DT
 XX Human glioblastoma cell RAS-related PATG29 protein.
 DE
 XX Phosphodiesterase; dunce-like phosphodiesterase; PDE; DPD; CAMP;
 KW RAS-related protein; immunoreactive; detection; genetic defect;
 KW bronchodilation; increased myocardial contractility; anti-inflammation.
 XX
 OS Homo sapiens.
 XX
 XX US5977305-A.
 FN
 XX
 XX 02-NOV-1999.
 PD
 XX
 XX 07-JUN-1995; 95US-00474379.
 PF
 XX
 XX 20-APR-1990; 90US-00511715.
 PR 19-APR-1991; 91US-00688352.
 PR 01-MAR-1994; 94US-00206188.
 XX
 XX (COLD-) COLD SPRING HARBOR LAB.
 PA
 XX
 XX Colicelli JJ, Wigler MH;
 PI
 XX WPI; 1999-619709/53.
 DR
 XX N-PSDB; AAZ32246.
 XX
 XX New isolated RAS-related polypeptides and mammalian cyclic nucleotide
 PT phosphodiesterases, used for screening for agents which can modify
 PT complement or suppress genetic defects.
 PT
 PS Claim 1; Col 119-122; 145pp; English.
 XX
 XX The present invention describes new isolated RAS-related polypeptides and
 CC mammalian cyclic nucleotide phosphodiesterases (PDEs). RAS-related
 CC polypeptides are capable of complementing a defective RAS function in
 CC yeast. The products can be used for screening for agents which can
 CC modify, complement or suppress a genetic defect in a biochemical pathway
 CC in which CAMP participates, or in a biochemical pathway which is
 CC controlled, directly or indirectly, by a RAS protein and other proteins
 CC affecting cell growth and maintenance. Developing agents that will
 CC selectively act upon PDEs is directed toward reproducing the desirable
 CC effects of cyclic nucleotides, e.g. bronchodilation, increased myocardial
 CC contractility, anti-inflammation, yet without causing the undesirable
 CC effects, e.g. increased heart rate or enhanced lipolysis. The products
 CC can also be used for therapeutic, diagnostic and prognostic uses.
 CC AAZ32229 to AAZ32285, and AAY49803 to AAY49830, represent sequences used
 CC in the exemplification of the present invention
 XX
 XX Sequence 369 AA;

Query Match 100.0%; Score 1747; DB 2; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.3e-134;

Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSEAEETQPPAAPAAPALSAADTKPOTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
 |||||
 DB 46 MSSEAEETQPPAAPAAPALSAADTKPOTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 105
 |||||
 QY 61 GTVKWNNVNGVGFNRNDTKEDVVFHOTATKKNPKYLRVSGDGTVEFDVVEGEGKA 120
 |||||
 DB 106 GTVKWNNVNGVGFNRNDTKEDVVFHOTATKKNPKYLRVSGDGTVEFDVVEGEGKA 165
 |||||
 QY 121 EAANYTGPVGVPVQGSKYAADRNHYRRYRRRPPYRRPQYNNYQNSSEGEKNEGSESAPEG 180
 |||||
 DB 166 EAANYTGPVGVPVQGSKYAADRNHYRRYRRRPPYRRPQYNNYQNSSEGEKNEGSESAPEG 225
 |||||
 QY 181 QAOQRPPYRRRPPYRRPGRPOYSNPPVQGVMEGADNCGAGEQGRPVRRQNNYRG 240
 |||||
 DB 226 QAOQRPPYRRRPPYRRPGRPOYSNPPVQGVMEGADNCGAGEQGRPVRRQNNYRG 285
 |||||
 QY 241 YRPRFRGPPRQROPREDGNEEDKENQDGTQGGQPPORRYRRNFYRRRRPENPKPDG 300
 |||||
 DB 286 YRPRFRGPPRQROPREDGNEEDKENQDGTQGGQPPORRYRRNFYRRRRPENPKPDG 345
 |||||
 QY 301 KETKAADPPAENSAPAEQGGAE 324
 |||||
 DB 346 KETKAADPPAENSAPAEQGGAE 369
 |||||
 RESULT 6
 AAB20625
 ID AAB20625 standard; protein; 369 AA.
 XX
 AC AAB20625;
 XX
 XX 14-DEC-2000 (first entry)
 DT
 XX
 XX PATG29 human glioblastoma cell insert protein sequence SEQ ID NO:32.
 DE
 XX Detection; mammalian gene; Yeast; microorganism; identification;
 KW phenotype; characteristic; dunce-like phosphodiesterase; PDE; RAS;
 KW RAS-related protein; genetic defect; hybridisation; probe.
 XX
 XX Homo sapiens.
 OS
 OS Schizosaccharomyces pombe.
 XX
 XX US6100025-A.
 FN
 XX
 XX 08-AUG-2000.
 PD
 XX
 XX 01-MAR-1994; 94US-00206188.
 PF
 XX
 XX 20-APR-1990; 90US-00511715.
 PR 19-APR-1991; 91US-00688352.
 XX
 XX (COLD-) COLD SPRING HARBOR LAB.
 PA
 XX
 XX Colicelli JJ, Wigler MH;
 PI
 XX WPI; 2000-531664/48.
 DR
 XX N-PSDB; AAZ88181.
 XX
 XX Novel isolated DNA encoding a mammalian cyclic nucleotide
 PT phosphodiesterase is present in plasmids pPDE46, pPDE43 or pPDE339 and is
 PT used to modify a genetic defect in a biochemical pathway in which CAMP
 PT participates.
 XX
 XX Example 1; Col 125-128; 145pp; English.
 PS
 XX The present invention describes a purified and isolated DNA (I) which
 CC encodes a mammalian cyclic nucleotide phosphodiesterase and is an insert
 CC present in the plasmids pPDE46 (ATCC 69552), pPDE43 (ATCC 69551) or
 CC pPDE339 (ATCC 69550). The DNA molecules are used to modify, complement or
 CC suppress a genetic defect in a biochemical pathway in which CAMP
 CC participates and are also used as hybridisation probes. The present

CC invention also describes methods for detecting mammalian genes encoding
CC proteins which can function in microorganisms, particularly yeast, to
CC modify, complement, or suppress a genetic defect associated with an
CC identifiable phenotypic alteration or characteristic in the
CC microorganism. AAA88162 to AAA88218 and AAB29614 to AAB20640 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 369 AA;

Query Match 100.0%; Score 1747; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.3e-134;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSEATQPPAAPPAALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
DB 46 MSSEATQPPAAPPAALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 105
QY 61 GTVKWNVNRYGGINRNDTKEDVFVHQTAKKNPKYLSVGDGETVEFDVVEGKGA 120
DB 106 GTVKWNVNRYGGINRNDTKEDVFVHQTAKKNPKYLSVGDGETVEFDVVEGKGA 165
QY 121 EAAVNTGPGVPGVQGSFYADRNHYRYPYRRPQYNNQYNSSEKNGESAPEG 180
DB 166 EAAVNTGPGVPGVQGSFYADRNHYRYPYRRPQYNNQYNSSEKNGESAPEG 225
QY 181 QAOQRYPYRRPFPYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 240
DB 226 QAOQRYPYRRPFPYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 285
QY 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNRYRRRPNPKPDG 300
DB 286 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNRYRRRPNPKPDG 345
QY 301 KETKAADPPAENSAPAEQGGAE 324
DB 346 KETKAADPPAENSAPAEQGGAE 369

RESULT 7
AA016411
ID AA016411 standard; protein; 384 AA.
AC AA016411;
XX
XX
DT 10-APR-2003 (first entry)
XX
DE Human nucleic acid-associated protein (NAAP) - SEQ ID No 8.
XX
XX Human; nucleic acid-associated protein; NAAP; arteriosclerosis;
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS;
KW cancer; developmental disorder; renal tubular acidosis; anaemia; asthma;
KW mental retardation; neurological disorder; Alzheimer's disease; epilepsy;
KW Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy;
KW Crohn's disease; transgenic animal; animal model.
XX
OS Homo sapiens.
XX
XX WO2003000864-A2.
FN
PD 03-JAN-2003.
XX
XX 20-JUN-2002; 2002WO-US021179.
PF
XX 22-JUN-2001; 2001US-0300518P.
PR
PR 29-JUN-2001; 2001US-0301787P.
PR 29-JUN-2001; 2001US-0301792P.
PR 29-JUN-2001; 2001US-0301892P.
PR 29-JUN-2001; 2001US-0301893P.
PR 06-JUL-2001; 2001US-0303405P.
PR 06-JUL-2001; 2001US-0303442P.
PR 15-MAR-2002; 2002US-0364438P.
XX
XX (INCY-) INCYTE GENOMICS INC.

XX Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM;
PI Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe IO;
PI Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Baughn MR;
PI Borowsky ML, Yao MG, Walla NK, Bandman O, Lal PG, Becha SD, Lee SY;
PI Richardson TW, Elliott VS, Luo W, Tang VT, Zebartadian Y, Lu Y;
XX
DR WPI: 2003-201420/19.
DR N-PSDB; AAL51561.
XX
PT New nucleic acid-associated proteins and polynucleotides, useful for
PT diagnosing, treating or preventing cell proliferative (e.g. cancer),
PT neurological (e.g. epilepsy or Parkinson's disease), or autoimmune
PT disorders (e.g. AIDS).
XX
PS Claim 1; Page 222-223; 312pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human
CC nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
CC the invention are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of NAAP, such as: cell proliferative
CC disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis
CC or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia
CC or mental retardation); neurological disorders (e.g. Alzheimer's disease,
CC Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders
CC (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of
CC the invention are useful for creating transgenic animals to model human
CC disease. The present amino acid sequence represents a human nucleic acid-
CC associated protein of the invention
XX
SQ Sequence 384 AA;

Query Match 99.8%; Score 1743; DB 6; Length 384;
Best Local Similarity 99.7%; Pred. No. 1.2e-133;
Matches 323; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSEATQPPAAPPAALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
DB 61 MSSEATQPPAAPPAALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 120
QY 61 GTVKWNVNRYGGINRNDTKEDVFVHQTAKKNPKYLSVGDGETVEFDVVEGKGA 120
DB 121 GTVKWNVNRYGGINRNDTKEDVFVHQTAKKNPKYLSVGDGETVEFDVVEGKGA 180
QY 121 EAAVNTGPGVPGVQGSFYADRNHYRYPYRRPQYNNQYNSSEKNGESAPEG 180
DB 181 EAAVNTGPGVPGVQGSFYADRNHYRYPYRRPQYNNQYNSSEKNGESAPEG 240
QY 181 QAOQRYPYRRPFPYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 240
DB 241 QAOQRYPYRRPFPYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 300
QY 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNRYRRRPNPKPDG 300
DB 301 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNRYRRRPNPKPDG 360
QY 301 KETKAADPPAENSAPAEQGGAE 324
DB 361 KETKAADPPAENSAPAEQGGAE 384

RESULT 8
AAW12827
ID AAW12827 standard; protein; 322 AA.
XX
AC AAW12827;
XX
DT 08-JAN-1998 (first entry)
XX
DE Rat TSEP-1 protein.
XX
XX Promoter; PD1; major histocompatibility complex; MHC Class I molecule;
KW mammalian cell; regulator; autoimmune disease; transplant rejection;
KW

therapy; non-thyroid autoimmune disease; Sox-4; TSEP-1 protein.

XX OS Rattus rattus. 59 GTVKWFWNRNGVGFIRNDTKEDVFVHQTAKKNPKYLSVGDGETVEFDVVEGEKGA 118
XX FH Key Location/Qualifiers 121 EAANTGFGVPGVQGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEKNGESASEG 180
XX FT Misc-difference 148..150 /note= "possible nuclear localisation signal" 119 EAANTGFGVPGVQGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEKNGESASEG 178
XX FT Misc-difference 183..190 /note= "possible nuclear localisation signal" 181 OAQQRPPYRRRRFPYNNRRPYGRRPQYSNPPVQGVNVEGADNCGAGGQGRPVQNNMYRG 240
XX FT Misc-difference 197..203 /note= "possible nuclear localisation signal" 179 QAQQRPPYRRRRFPYNNRRPYARRPQYSNPPVQGVNVEGADNCGAGGQGRPVQNNMYRG 238
XX FT Misc-difference 240..245 /note= "possible nuclear localisation signal" 241 YRPRFRGPPRQRPREDGNEEDKENQGDETQGQOPPORRYRRNPNYRRRRPENPKPDG 300
XX FT Misc-difference 277..281 /note= "possible nuclear localisation signal" 239 YRPRFRGPPRQRPREDGNEEDKENQGDETQGQOPPORRYRRNPNYRRRRPENPKPDG 298
XX FT Misc-difference 286..289 /note= "possible nuclear localisation signal" 301 KETKAADPPAENSSAPEAEQGGAE 324
XX FT Misc-difference 286..289 /note= "possible nuclear localisation signal" 299 KETKAADPPAENSSAPEAEQGGAE 322
XX EN WO9707404-A1.
XX XX 27-FEB-1997.
XX XX 21-AUG-1996; 96WO-US013715.
XX XX 21-AUG-1995; 95US-00503525.
XX XX (USSH) US SEC DEPT HEALTH.
XX Kohn L, Singer DS, Saji M, Giuliani C, Shong M, Suzuki K;
XX Ohmori M;
XX WPI; 1997-165448/15.
XX N-PSDB; AAT59845.
XX Identification of drugs which modulate MHC Class I expression - used in
XX the prevention and treatment of autoimmune disease and transplant
XX rejection.
XX Claim 23; Fig 38b; 273pp; English.
XX This sequence represents the rat TSEP-1 protein. This protein is a Y-box
XX protein, and can be used in the method of the invention. The method of
XX the invention is for assessing the ability, or therapeutic potential, of
XX a drug to suppress expression of MHC Class I molecules by measuring
XX altered binding of a mammalian cell protein extract to an MHC Class I
XX regulatory nucleic acid sequence or functional equivalent. The method
XX comprises treating the mammalian cells with the drug. Protein extract is
XX then obtained from the cells and is combining with a regulatory nucleic
XX acid sequence to allow formation of at least one complex between the
XX protein and nucleic acid. Finally, the formation of the complex is
XX detected where altered complex formation indicates the drugs potential
XX in treating autoimmune disease or transplant rejection. The other methods
XX of the invention are for assessing the ability of a drug to suppress
XX expression of MHC Class I molecules, for assessing the therapeutic
XX potential of a candidate drug, and for assessing the therapeutic
XX potential of a candidate drug for treating autoimmune disease or
XX transplant rejection. The methods are used to identify nucleic acids and
XX other compounds capable of MHC Class I suppression which may be used in
XX the prevention or treatment of transplant rejection in a mammal, or the
XX treatment of a non-thyroid autoimmune disease. The antibodies of the
XX invention may be used to detect either Sox-4 or TSEP-1 proteins
XX Sequence 322 AA;

Db 59 GTVKWFWNRNGVGFIRNDTKEDVFVHQTAKKNPKYLSVGDGETVEFDVVEGEKGA 118
QY 121 EAANTGFGVPGVQGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEKNGESASEG 180
Db 119 EAANTGFGVPGVQGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEKNGESASEG 178
QY 181 OAQQRPPYRRRRFPYNNRRPYGRRPQYSNPPVQGVNVEGADNCGAGGQGRPVQNNMYRG 240
Db 179 QAQQRPPYRRRRFPYNNRRPYARRPQYSNPPVQGVNVEGADNCGAGGQGRPVQNNMYRG 238
QY 241 YRPRFRGPPRQRPREDGNEEDKENQGDETQGQOPPORRYRRNPNYRRRRPENPKPDG 300
Db 239 YRPRFRGPPRQRPREDGNEEDKENQGDETQGQOPPORRYRRNPNYRRRRPENPKPDG 298
QY 301 KETKAADPPAENSSAPEAEQGGAE 324
Db 299 KETKAADPPAENSSAPEAEQGGAE 322
RESULT 9
ABB80304
ID ABB80304 standard; protein; 322 AA.
XX AC ABB80304;
XX DT 15-JAN-2004 (first entry)
XX DE Rat Y-box protein.
XX KW Protein tyrosine phosphatase 1B; PTP1B; insulin receptor kinase; IRK;
XX KW Protein tyrosine kinase; diabetes; obesity; Y-box protein; YB-1;
XX KW impaired glucose tolerance.
XX OS Rattus norvegicus.
XX PN WO2003076634-A2.
XX PD 18-SEP-2003.
XX PF 12-MAR-2003; 2003WO-EP002552.
XX PR 12-MAR-2002; 2002US-0363787P.
XX PR 20-DEC-2002; 2002US-0435587P.
XX PR 11-MAR-2003; 2003US-00388215.
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX (TONK/) TONKS N K.
XX Fukada T;
XX WPI; 2003-758826/71.
XX New isolated polynucleotide useful for treating protein tyrosine
XX phosphatase (PTP1B)-associated disorders (e.g. diabetes, obesity or
XX impaired glucose tolerance) and for identifying agents capable of
XX altering PTP1B expression.
XX Claim 19; Page 113-14; 115pp; English.
XX This sequence represents a rat Y-box protein. This protein binds to the Y
XX -box protein (YB-1) binding site. Y-box proteins are capable of
XX interacting with DNA and RNA and possess a conserved domain of approx. 70
XX amino acids termed the cold-shock domain, which is capable of binding to
XX a DNA "Y-box" sequence (ATTGG). This sequence is useful in treating PTP1B
XX -associated disorders or conditions associated with defects in biological
XX signal transduction in cells, such as diabetes, obesity, impaired glucose
XX tolerance and other metabolic disorders. This sequence may also be used
XX in identifying agents capable of altering PTP1B expression
XX Sequence 322 AA;

Query Match

97.7%; Score 1707; DB 7; Length 322;

Query Match 97.7%; Score 1707; DB 2; Length 322;

Best Local Similarity 98.5%; Pred. No. 8.2e-131; Indels 2; Gaps 1;
Matches 319; Conservative 1; Mismatches 2;

QY 1 MSSEAEATQPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKYL 60
Db 1 MSSEAEATQPPAAP--AAALSAADTKPGTSGAGSGGPGGLTSAAPAGGDKKVIATKYL 58
QY 61 GTVKWFWNRNGVGFIRNDTKEDVFVHQTAKKNPKYLSVGDGETVEFDVVEGEKGA 120

Best Local Similarity 98.5%; Pred. No. 8.2e-131;
Matches 319; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MSSEAEATQPPAAPAAPALSAADTKPGTTGSGAGSGPGGLTSAAPAGGDKKVIATKVL 60
DB 1 MSSEAEATQPPAAP--AAALSAADTKPGTSGAGSGPGGLTSAAPAGGDKKVIATKVL 58
QY 61 GTVKWNVNRNGYGFINRNDTKEDVHFQTAIKKNNPKYLSVGDGETVEFDVVEGEKGA 120
DB 59 GTVKWNVNRNGYGFINRNDTKEDVHFQTAIKKNNPKYLSVGDGETVEFDVVEGEKGA 118
QY 121 EAAAVTGGPGVPVQGSKYAADRNHYRYPYRRPQYNSNPVQGEVMEGADNQGAGGQGRPVQNNMYRG 180
DB 119 EAAAVTGGPGVPVQGSKYAADRNHYRYPYRRPQYNSNPVQGEVMEGADNQGAGGQGRPVQNNMYRG 178
QY 181 QAQORRPPYRRRFPYMYRRPQYNSNPVQGEVMEGADNQGAGGQGRPVQNNMYRG 240
DB 179 QAQORRPPYRRRFPYMYRRPQYNSNPVQGEVMEGADNQGAGGQGRPVQNNMYRG 238
QY 241 YRFRFRGPPRQOPREDGNEEDKENQDGTGQOPPORRYRNFNRRRPNPKPDG 300
DB 239 YRFRFRGPPRQOPREDGNEEDKENQDGTGQOPPORRYRNFNRRRPNPKPDG 298
QY 301 KETKAADPPAENSAPAEQGGAE 324
DB 299 KETKAADPPAENSAPAEQGGAE 322

RESULT 10
ADE61260
ID ADE61260 standard; protein; 322 AA.
AC ADE61260;
XX 29-JAN-2004 (first entry)
XX Rat Protein: P27817, SEQ ID NO 7178.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P27817.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 322 AA;

Query Match 97.7%; Score 1707; DB 7; Length 322;
Best Local Similarity 98.5%; Pred. No. 8.2e-131;
Matches 319; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MSSEAEATQPPAAPAAPALSAADTKPGTTGSGAGSGPGGLTSAAPAGGDKKVIATKVL 60
DB 1 MSSEAEATQPPAAP--AAALSAADTKPGTSGAGSGPGGLTSAAPAGGDKKVIATKVL 58
QY 61 GTVKWNVNRNGYGFINRNDTKEDVHFQTAIKKNNPKYLSVGDGETVEFDVVEGEKGA 120
DB 59 GTVKWNVNRNGYGFINRNDTKEDVHFQTAIKKNNPKYLSVGDGETVEFDVVEGEKGA 118
QY 121 EAAAVTGGPGVPVQGSKYAADRNHYRYPYRRPQYNSNPVQGEVMEGADNQGAGGQGRPVQNNMYRG 180
DB 119 EAAAVTGGPGVPVQGSKYAADRNHYRYPYRRPQYNSNPVQGEVMEGADNQGAGGQGRPVQNNMYRG 178
QY 181 QAQORRPPYRRRFPYMYRRPQYNSNPVQGEVMEGADNQGAGGQGRPVQNNMYRG 240
DB 179 QAQORRPPYRRRFPYMYRRPQYNSNPVQGEVMEGADNQGAGGQGRPVQNNMYRG 238
QY 241 YRFRFRGPPRQOPREDGNEEDKENQDGTGQOPPORRYRNFNRRRPNPKPDG 300
DB 239 YRFRFRGPPRQOPREDGNEEDKENQDGTGQOPPORRYRNFNRRRPNPKPDG 298
QY 301 KETKAADPPAENSAPAEQGGAE 324
DB 299 KETKAADPPAENSAPAEQGGAE 322

RESULT 11
ADD48835
ID ADD48835 standard; protein; 322 AA.
XX
XX AC ADD48835;
XX 29-JAN-2004 (first entry)
XX
XX DE Rat Protein A23677, SEQ ID NO 14545.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX
XX PN WO2003016475-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; A23677.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 322 AA;
 Query Match 97.7%; Score 1707; DB 7; Length 322;
 Best Local Similarity 98.5%; Pred. No. 8.2e-131;
 Matches 319; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
 QY 1 MSSEAEFCQPPAAPALSAADTKPTGSGAGSGGPGGLTSAAPAGDKKVIATKYL 60
 DB 1 MSSEAEFCQPPAAPALSAADTKPTGSGAGSGGPGGLTSAAPAGDKKVIATKYL 58
 QY 61 GTVKWFVNRNGYGFINRNDTKEDVFVQHTAIKNNPKYLSRSGDGETVEFDVVEGEKA 120
 DB 59 GTVKWFVNRNGYGFINRNDTKEDVFVQHTAIKNNPKYLSRSGDGETVEFDVVEGEKA 118
 QY 121 EAAVNTGPGVPGVQSGKYAADRHRYRPRRPPRYQNYQNSGSGKNEGSAPGG 180
 DB 119 EAAVNTGPGVPGVQSGKYAADRHRYRPRRPPRYQNYQNSGSGKNEGSAPGG 178
 QY 181 QAOQRYYRRRRPPPYMYRRPYGRRPOYSNPPVQGVMEAGNQAGEOGRPVQRMVYRG 240
 DB 179 QAOQRYYRRRRPPPYMYRRPYGRRPOYSNPPVQGVMEAGNQAGEOGRPVQRMVYRG 238
 QY 241 YRFRFRGPPRQRPREDGNEEDKENQDGTQCCQPPQRRYRNFNRYRRRRPENPKPDG 300
 DB 239 YRFRFRGPPRQRPREDGNEEDKENQDGTQCCQPPQRRYRNFNRYRRRRPENPKPDG 298
 QY 301 KETKAADPPAENSSAPEAEOGGAE 324

DB 299 KETKAADPPAENSSAPEAEOGGAE 322
 RESULT 12
 ADE61263
 ID ADE61263 standard; protein; 322 AA.
 XX
 AC ADE61263;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein P27817, SEQ ID NO 7181.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; P27817.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 322 AA;
 Query Match 97.7%; Score 1707; DB 7; Length 322;
 Best Local Similarity 98.5%; Pred. No. 8.2e-131;
 Matches 319; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Matches 319; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MSSEATQPPAAPAALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVL 60
 DB 1 MSSEATQPPAAPA--AALSAADTKPGTSGAGSGGPGGLTSAAPAGGDKKVIATKVL 58
 QY 61 GTVKFNVNRYGFGFINRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGEKGA 120
 DB 59 GTVKFNVNRYGFGFINRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGEKGA 118
 QY 121 EAAANTGCGVPVQGSKYAADRNHYRYPERRGPPNNYQNYQNSSEKNEGSAPG 180
 DB 119 EAAANTGCGVPVQGSKYAADRNHYRYPERRGPPNNYQNYQNSSEKNEGSAPG 178
 QY 181 QAQORRYRRRRFPFYMRPYYGRPPQYSNPPVQGEVMEGADNQGAGEQGRPVQRNNYRG 240
 DB 179 QAQORRYRRRRFPFYMRPYYGRPPQYSNPPVQGEVMEGADNQGAGEQGRPVQRNNYRG 238
 QY 241 YRFRFRGPPRQPRQPRDGNEDKENQDGTQGGPPORRYRNNYRNRPPENPKPDG 300
 DB 239 YRFRFRGPPRQPRQPRDGNEDKENQDGTQGGPPORRYRNNYRNRPPENPKPDG 298
 QY 301 KETKAADPPAENSAPAEQGGAE 324
 DB 299 KETKAADPPAENSAPAEQGGAE 322

RESULT 13
 ABB57039
 ID ABB57039 standard; protein; 322 AA.
 AC ABB57039;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:52.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX
 OS Mus musculus.
 XX
 FN WO200188188-A2.
 XX
 PD 22-NOV-2001.
 XX
 FF 18-MAY-2001; 2001WO-JP004192.
 XX
 FR 18-MAY-2000; 2000JP-00145977.
 XX
 PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 DR WPI; 2002-034733/04.
 XX
 DR N-PSDB; ABI99233.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX
 PS Claim 2; Page 171-172; 2690pp; English.
 XX
 CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (i) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (i). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression

CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 322 AA;

Query Match 97.4%; Score 1701; DB 5; Length 322;
 Best Local Similarity 98.1%; Pred. No. 2.5e-130;
 Matches 318; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 MSSEATQPPAAPAALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVL 60
 DB 1 MSSEATQPPAAP--AALSAADTKPGTSGAGSGGPGGLTSAAPAGGDKKVIATKVL 58
 QY 61 GTVKFNVNRYGFGFINRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGEKGA 120
 DB 59 GTVKFNVNRYGFGFINRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGEKGA 118
 QY 121 EAAANTGCGVPVQGSKYAADRNHYRYPERRGPPNNYQNYQNSSEKNEGSAPG 180
 DB 119 EAAANTGCGVPVQGSKYAADRNHYRYPERRGPPNNYQNYQNSSEKNEGSAPG 178
 QY 181 QAQORRYRRRRFPFYMRPYYGRPPQYSNPPVQGEVMEGADNQGAGEQGRPVQRNNYRG 240
 DB 179 QAQORRYRRRRFPFYMRPYYGRPPQYSNPPVQGEVMEGADNQGAGEQGRPVQRNNYRG 238
 QY 241 YRFRFRGPPRQPRQPRDGNEDKENQDGTQGGPPORRYRNNYRNRPPENPKPDG 300
 DB 239 YRFRFRGPPRQPRQPRDGNEDKENQDGTQGGPPORRYRNNYRNRPPENPKPDG 298
 QY 301 KETKAADPPAENSAPAEQGGAE 324
 DB 299 KETKAADPPAENSAPAEQGGAE 322

RESULT 14
 ABB80303
 ID ABB80303 standard; protein; 322 AA.
 XX
 AC ABB80303;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Mouse Y-box protein.
 XX
 KW Protein tyrosine phosphatase 1B; FTYB; insulin receptor kinase; IRK;
 KW protein tyrosine kinase; diabetes; obesity; Y-box protein; YB-1;
 KW impaired glucose tolerance.
 XX
 OS Mus musculus.
 XX
 FN WO2003076634-A2.
 XX
 PD 18-SEP-2003.
 XX
 FF 12-MAR-2003; 2003WO-EP002552.
 XX
 PR 12-MAR-2002; 2002US-0363787P.
 PR 20-DEC-2002; 2002US-0435587P.
 PR 11-MAR-2003; 2003US-00388215.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (TONK/) TONKS N K.
 XX
 PI Fukada T;
 DR WPI; 2003-756826/71.
 XX
 PT New isolated polynucleotide useful for treating protein tyrosine
 PT phosphatase (PTP)B-associated disorders (e.g. diabetes, obesity or
 PT impaired glucose tolerance) and for identifying agents capable of

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OM protein - protein search, using sw model
Run on: August 25, 2004, 00:21:45 ; Search time 32 Seconds
(without alignments)
522.713 Million cell updates/sec

Title: US-10-028-415-40
Perfect score: 1747
Sequence: 1 MSSEATQPPAAPAPAL.....AADPPAENSSAPAEQGGAE 324

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1747	100.0	369	1	US-07-688-352C-32
2	1747	100.0	369	2	US-08-474-379C-32
3	1747	100.0	369	3	US-09-146-249A-32
4	1747	100.0	369	3	US-08-206-188B-32
5	1747	100.0	369	5	PCT-US91-02714-31
6	384	22.0	74	1	US-08-203-806B-13
7	384	22.0	74	4	US-09-017-754A-13
8	172	9.8	131	4	US-09-489-039A-13476
9	163.5	9.6	82	4	US-09-134-001C-5476
10	164.5	9.4	116	4	US-09-252-991A-19664
11	163.5	9.4	86	4	US-09-107-532A-5955
12	163	9.3	69	1	US-08-203-806B-4
13	163	9.3	69	1	US-08-203-806B-9
14	163	9.3	69	4	US-09-017-754A-4
15	163	9.3	69	4	US-09-017-754A-9
16	163	9.3	73	4	US-09-489-039A-14126
17	163	9.3	507	4	US-09-252-991A-17308
18	162.5	9.3	214	4	US-09-252-991A-29350
19	162	9.3	70	4	US-08-516-667-80
20	160.5	9.2	94	4	US-09-540-236-2432
21	159.5	9.1	79	4	US-09-134-001C-3081
22	158	9.0	73	4	US-09-543-681A-4308
23	158	9.0	99	4	US-09-543-681A-5351
24	156.5	9.0	481	4	US-09-252-991A-17707
25	155	8.9	82	4	US-09-543-681A-7943
26	152.5	8.7	1075	4	US-09-252-991A-18387
27	152	8.7	71	1	US-08-203-806B-2

28	152	8.7	71	1	US-08-203-806B-8	Sequence 8, Appl
29	152	8.7	71	4	US-09-017-754A-2	Sequence 2, Appl
30	152	8.7	71	4	US-09-017-754A-8	Sequence 8, Appl
31	152	8.7	71	4	US-09-516-667-81	Sequence 81, Appl
32	152	8.7	71	4	US-09-293-427-4	Sequence 4, Appl
33	151.5	8.7	71	4	US-09-328-352-4376	Sequence 4376, Ap
34	151.5	8.7	73	4	US-09-107-532A-6235	Sequence 6235, Ap
35	150.5	8.6	352	4	US-09-252-991A-24482	Sequence 24482, A
36	150.5	8.6	705	4	US-09-252-991A-30792	Sequence 30792, A
37	150	8.6	70	1	US-08-203-806B-7	Sequence 7, Appl
38	150	8.6	70	4	US-09-017-754A-7	Sequence 7, Appl
39	150	8.6	70	4	US-09-017-754A-20	Sequence 20, Appl
40	150	8.6	70	4	US-09-516-667-82	Sequence 82, Appl
41	150	8.6	72	4	US-09-489-039A-10823	Sequence 10823, A
42	150	8.6	1098	4	US-09-252-991A-20186	Sequence 20186, A
43	149	8.5	85	4	US-09-540-236-2549	Sequence 2549, Ap
44	148	8.5	720	4	US-09-252-991A-21881	Sequence 21881, A
45	147.5	8.4	396	4	US-09-252-991A-24697	Sequence 24697, A

ALIGNMENTS

RESULT 1
US-07-688-352C-32
; Sequence 32, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07688,352C
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-688-352C-32

Query Match 100.0%; Score 1747; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAEETQPPAAPALSAADTKGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVL 60
 Db 46 MSSEAEETQPPAAPALSAADTKGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVL 105
 QY 61 GTVKFNVNRNGYGFNRNDTKEDVFVHQTAKKONPKYLSRSGDGETVDFVVEGEKGA 120
 Db 106 GTVKFNVNRNGYGFNRNDTKEDVFVHQTAKKONPKYLSRSGDGETVDFVVEGEKGA 165
 QY 121 EAAVTGPGGVVQGSKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSESAPEG 180
 Db 166 EAAVTGPGGVVQGSKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSESAPEG 225
 QY 181 QAQORRPYRRRRFPYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQRNNYRG 240
 Db 226 QAQORRPYRRRRFPYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQRNNYRG 285
 QY 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFYRRRRPENPKPDG 300
 Db 286 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFYRRRRPENPKPDG 345
 QY 301 KETKAADPPAENSAPAEQGGAE 324
 Db 346 KETKAADPPAENSAPAEQGGAE 369

RESULT 2

US-08-474-379C-32
 ; Sequence 32, Application US/08474379C
 ; Patent No. 5977305
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
 ; TITLE OF INVENTION: PROCESSES
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive/6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,379C
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/206,188
 ; FILING DATE: 01-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/688,352
 ; FILING DATE: 19-APR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; REFERENCE/DOCKET NUMBER: 27866/32771
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 369 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein
 US-08-474-379C-32
 Query Match 100.0%; Score 1747; DB 2; Length 369;
 Best Local Similarity 100.0%; Pred. No. 1.1e-139;
 Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSEAEETQPPAAPALSAADTKGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVL 60
 Db 46 MSSEAEETQPPAAPALSAADTKGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVL 105
 QY 61 GTVKFNVNRNGYGFNRNDTKEDVFVHQTAKKONPKYLSRSGDGETVDFVVEGEKGA 120
 Db 106 GTVKFNVNRNGYGFNRNDTKEDVFVHQTAKKONPKYLSRSGDGETVDFVVEGEKGA 165
 QY 121 EAAVTGPGGVVQGSKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSESAPEG 180
 Db 166 EAAVTGPGGVVQGSKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSESAPEG 225
 QY 181 QAQORRPYRRRRFPYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQRNNYRG 240
 Db 226 QAQORRPYRRRRFPYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQRNNYRG 285
 QY 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFYRRRRPENPKPDG 300
 Db 286 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFYRRRRPENPKPDG 345
 QY 301 KETKAADPPAENSAPAEQGGAE 324
 Db 346 KETKAADPPAENSAPAEQGGAE 369

RESULT 3

US-09-146-249A-32
 ; Sequence 32, Application US/09146249A
 ; Patent No. 6069240
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; TITLE OF INVENTION: Processes
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/146,249A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 369 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear


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; MOLECULE TYPE: protein
US-09-146-249A-32

Query Match      100.0%; Score 1747; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSEAEETQPPAAPPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
DB 46 MSSEAEETQPPAAPPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 105
QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGEKGA 120
DB 106 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGEKGA 165
QY 121 EAAVNTGPGVPGVQSKYAADRHHYRRYPRRRGPPRRNYQNYQNSSEKNEGSESAPEG 180
DB 166 EAAVNTGPGVPGVQSKYAADRHHYRRYPRRRGPPRRNYQNYQNSSEKNEGSESAPEG 225
QY 181 QAOQRYYRRRRFPFYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQRNMYRG 240
DB 226 QAOQRYYRRRRFPFYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQRNMYRG 285
QY 241 YRPRFRGPPRQORPDGNEEDKENOGDETQGGQPPORRYRNFNRYRRRRPENPKPDG 300
DB 286 YRPRFRGPPRQORPDGNEEDKENOGDETQGGQPPORRYRNFNRYRRRRPENPKPDG 345
QY 301 KETKAADPPAENSSAPEAQGGAE 324
DB 346 KETKAADPPAENSSAPEAQGGAE 369
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RESULT 4
US-08-206-188B-32
; Sequence 32, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-206-188B-32

Query Match      100.0%; Score 1747; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSEAEETQPPAAPPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
DB 46 MSSEAEETQPPAAPPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 105
QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGEKGA 120
DB 106 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGEKGA 165
QY 121 EAAVNTGPGVPGVQSKYAADRHHYRRYPRRRGPPRRNYQNYQNSSEKNEGSESAPEG 180
DB 166 EAAVNTGPGVPGVQSKYAADRHHYRRYPRRRGPPRRNYQNYQNSSEKNEGSESAPEG 225
QY 181 QAOQRYYRRRRFPFYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQRNMYRG 240
DB 226 QAOQRYYRRRRFPFYMYRRPYGRPOYSNPPVQGEVMEGADNQGAGEQGRPVQRNMYRG 285
QY 241 YRPRFRGPPRQORPDGNEEDKENOGDETQGGQPPORRYRNFNRYRRRRPENPKPDG 300
DB 286 YRPRFRGPPRQORPDGNEEDKENOGDETQGGQPPORRYRNFNRYRRRRPENPKPDG 345
QY 301 KETKAADPPAENSSAPEAQGGAE 324
DB 346 KETKAADPPAENSSAPEAQGGAE 369

RESULT 5
PCT-US91-02714-31
; Sequence 31, Application PC/TUS9102714
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell,
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02714
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
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; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02714-31

Query Match 100.0%; Score 1747; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAETQPPAAPALSAADTKCTTSGAGSGPGGLTSAAPAGGDKVIATKVL 60
Db 46 MSSAETQPPAAPALSAADTKCTTSGAGSGPGGLTSAAPAGGDKVIATKVL 105
QY 61 GTVWFNVNRYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVDFVVEGEKGA 120
Db 106 GTVWFNVNRYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVDFVVEGEKGA 165
QY 121 EAAVNTGGGVVQGSKYAADRNHYRPRRGGPPRYNQYQNSSEGEKNGESAPEG 180
Db 166 EAAVNTGGGVVQGSKYAADRNHYRPRRGGPPRYNQYQNSSEGEKNGESAPEG 225
QY 181 QAQRRPYRRRRFPYRRPQYNSPPVOGEVMEGADNQGAGEQGRPVRRQNNYRG 240
Db 226 QAQRRPYRRRRFPYRRPQYNSPPVOGEVMEGADNQGAGEQGRPVRRQNNYRG 285
QY 241 YRPRFRGGPPRQRPREDGNEEDKENQDETQGGQPPQRRYRNFNRRRPNPKPDG 300
Db 286 YRPRFRGGPPRQRPREDGNEEDKENQDETQGGQPPQRRYRNFNRRRPNPKPDG 345
QY 301 KETKAADPPAENSSAPAEQGGAE 324
Db 346 KETKAADPPAENSSAPAEQGGAE 369

RESULT 6
US-08-203-806B-13
; Sequence 13, Application US/08203806B
; Patent No. 5714575
; GENERAL INFORMATION:
; APPLICANT: Inouye, Masayori
; APPLICANT: Jones, Pamela
; APPLICANT: Etchegaray, Jean-Pierre
; APPLICANT: Weinig, Jian
; APPLICANT: Pollitt, N. Stephen
; APPLICANT: Goldstein, Joel
; TITLE OF INVENTION: Nucleic Acid Sequences, Stress-induced
; TITLE OF INVENTION: Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,806B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 377,5998P
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; TELEX: 834809 WEISTAK
; INFORMATION FOR SEQ ID NO: 13:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-203-806B-13

Query Match 22.0%; Score 384; DB 1; Length 74;
Best Local Similarity 98.6%; Pred. No. 1.6e-25;
Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 IATKVLGVKFWNVNRYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVDFDV 114
Db 1 IATKVLGVKFWNVNRYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVDFDV 60
QY 115 EGEKGAEEAANVTGP 128
Db 61 EGEKGAEEAANVTGP 74

RESULT 7
US-09-017-754A-13
; Sequence 13, Application US/09017754A
; Patent No. 6333191
; GENERAL INFORMATION:
; APPLICANT: Inouye, Masayori
; APPLICANT: JONES, PAMELA
; APPLICANT: ETCHEGARAY, JEAN-PIERRE
; APPLICANT: WEINING, JIANG
; APPLICANT: POLLITT, N. STEPHEN
; APPLICANT: GOLDSTEIN, JOEL
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES, STRESS-INDUCED
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCHNADDER, HARRISON, SEGAL & LEWIS, LLP
; STREET: 1600 Market Street, Suite 3600
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,754A
; FILING DATE: 03-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 1113-cip2-div-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-751-2427
; TELEFAX: 215-751-2658
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-017-754A-13

Query Match 22.0%; Score 384; DB 4; Length 74;
Best Local Similarity 98.6%; Pred. No. 1.6e-25;
Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 IATKVLGVKFWNVNRYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVDFDV 114

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Db 1 IATKVLGTWKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDV 60
 QY 115 EGEKGAEAAVNTGP 128
 Db 61 EGEKGAEAAVNTGP 74

RESULT 8
 US-09-489-039A-13476
 ; Sequence 13476, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.204001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13476
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-13476

Query Match 9.8%; Score 172; DB 4; Length 131;
 Best Local Similarity 43.2%; Pred. No. 2.5e-07;
 Matches 32; Conservative 15; Mismatches 23; Indels 4; Gaps 1;
 QY 52 KVIATKVLGTWKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEF 111
 Db 59 KVIATKVLGTWKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEF 114
 QY 112 DVVEGEKGAEEAANV 125
 Db 115 EITNGAKGPSAANV 128

RESULT 9
 US-09-134-001C-5476
 ; Sequence 5476, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 5476
 ; LENGTH: 82
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-5476

Query Match 9.6%; Score 168.5; DB 4; Length 82;
 Best Local Similarity 52.3%; Pred. No. 2.8e-07;
 Matches 34; Conservative 13; Mismatches 13; Indels 5; Gaps 2;
 QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 120
 Db 20 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 74
 QY 121 EAAV 125

Db 75 QAAV 79
 RESULT 10
 US-09-252-991A-19664
 ; Sequence 19664, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19664
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19664

Query Match 9.4%; Score 164.5; DB 4; Length 116;
 Best Local Similarity 47.9%; Pred. No. 9.4e-07;
 Matches 35; Conservative 14; Mismatches 19; Indels 5; Gaps 2;
 QY 54 VIATKVLGTWKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDV 113
 Db 47 VMADEVCVTKWENDAKGYGFIQR-DSGDFVHVHRAIRGEGH---RSLVEGQKVEFSV 101
 QY 114 VEGEKGAEEAANV 126
 Db 102 IQQKGLQAEVDS 114

RESULT 11
 US-09-107-532A-5955
 ; Sequence 5955, Application US/09107532A
 ; Patent No. 6583275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; NUMBER OF SEQUENCES: 7310
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02354
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-ROM ISO9660
 ; COMPUTER: PC
 ; OPERATING SYSTEM: <Unknown>
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107,532A
 ; FILING DATE: 30-Jun-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/085,598
 ; FILING DATE: 14 May 1998
 ; APPLICATION NUMBER: 60/051571
 ; FILING DATE: July 2, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ariniello, Pamela Denek
 ; REGISTRATION NUMBER: 40,489
 ; REFERENCE/DOCKET NUMBER: GTC-012
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781)893-5007

```

; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5955:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...86
; SEQUENCE DESCRIPTION: SEQ ID NO: 5955:
US-09-107-532A-5955

Query Match          9.4%; Score 163.5; DB 4; Length 86;
Best Local Similarity 40.5%; Pred. No. 7.8e-07;
Matches 30; Conservative 22; Mismatches 17; Indels 5; Gaps 2;

Qy 52 KVLATKVLGVNVRNGYGFNRNDTKEDVVFHQTAKKNPKYLSVGDGETVFEF 111
Db 4 RKVSAUTTGILVWFDNKGKGFISYDDT-EEIFVHFHFALEEG-----FKTLEENQVVEF 58

Qy 112 DWVEGEGAAAVNT 125
Db 59 EIIENRGTAQAAHV 72

RESULT 12
US-08-203-806B-4
; Sequence 4, Application US/08203806B
; Patent No. 5714575
; GENERAL INFORMATION:
; APPLICANT: Inouye, Masayori
; APPLICANT: Jones, Pamela
; APPLICANT: Etchegaray, Jean-Pierre
; APPLICANT: Weinig, Jian
; APPLICANT: Pollitt, N. Stephen
; APPLICANT: Goldstein, Joel
; TITLE OF INVENTION: Nucleic Acid Sequences, Stress-induced
; TITLE OF INVENTION: Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,806B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 377.5998P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; ORGANISM: Escherichia coli
US-08-203-806B-9

Query Match          9.3%; Score 163; DB 1; Length 69;
Best Local Similarity 44.9%; Pred. No. 6.6e-07;
Matches 31; Conservative 14; Mismatches 20; Indels 4; Gaps 1;

Qy 58 KVLGTWKVFNVRNGYGFNRNDTKEDVVFHQTAKKNPKYLSVGDGETVFEF 117
Db 3 KIKGVKWFNFKSGFGFITPADGSKDVVFHFSALQNG-----FKTLAEGQNVFEIQDQG 58

Qy 118 KGAEAAVNT 126
Db 59 KGPAAVVNT 67

RESULT 13
US-08-203-806B-9
; Sequence 9, Application US/08203806B
; Patent No. 5714575
; GENERAL INFORMATION:
; APPLICANT: Inouye, Masayori
; APPLICANT: Jones, Pamela
; APPLICANT: Etchegaray, Jean-Pierre
; APPLICANT: Weinig, Jian
; APPLICANT: Pollitt, N. Stephen
; APPLICANT: Goldstein, Joel
; TITLE OF INVENTION: Nucleic Acid Sequences, Stress-induced
; TITLE OF INVENTION: Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,806B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 377.5998P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; ORGANISM: Escherichia coli
US-08-203-806B-9

Query Match          9.3%; Score 163; DB 1; Length 69;
Best Local Similarity 44.9%; Pred. No. 6.6e-07;
Matches 31; Conservative 14; Mismatches 20; Indels 4; Gaps 1;

Qy 58 KVLGTWKVFNVRNGYGFNRNDTKEDVVFHQTAKKNPKYLSVGDGETVFEF 117
Db 3 KIKGVKWFNFKSGFGFITPADGSKDVVFHFSALQNG-----FKTLAEGQNVFEIQDQG 58

Qy 118 KGAEAAVNT 126
Db 59 KGPAAVVNT 67
```

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; PROTEINS AND USES THEOREF
;
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCHNADER, HARRISON, SEGAL & LEWIS, LLP
; STREET: 1600 Market Street, Suite 3600
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,754A
; FILING DATE: 03-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 1113-cip2-div-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-751-2427
; TELEFAX: 215-751-2658
;
; INFORMATION FOR SEQ ID NO: 9:
;-----
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-017-754A-9
;
Query Match          9.3%; Score 163; DB 4; Length 69;
Best Local Similarity 44.9%; Pred.No.'6.6e-07;
Matches 31; Conservative 14; Mismatches 20; Indels 4; Gaps 1;

Qy   58 KVLGTVKWNVRNGYGFIRNDTKEDVFVHOTAIKKONPKYLRSVGDTVEFDVVEGE 117
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    3 KIKGVKWKNESKGFGFITPADGSKDVFHFSAIQGNGL---FKTLAEQNVEFIQDQG 58
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Qy   118 KGAAEAAVV 126
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    59 KGPAAVNV 67
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Search completed: August 25, 2004, 00:27:41
Job time : 34 secs

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Sequence 142, App
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Sequence 221, App
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Sequence 39, App1
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Sequence 4161, Ap
Sequence 143, App
Sequence 62338, A
Sequence 40158, A
Sequence 40165, A
Sequence 42358, A
Sequence 41792, A
Sequence 42359, A
Sequence 41779, A
Sequence 41771, A
Sequence 256768, A
Sequence 41411, A
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Sequence 256772, A
Sequence 42357, A
Sequence 256774, A
Sequence 41777, A
Sequence 39486, A
Sequence 245, App
Sequence 256, App
Sequence 15394, A
Sequence 1041, Ap
Sequence 110, App

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2253	10	US-09-764-846-221
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2253	14	US-10-091-483-221
66	13	US-10-032-415-39
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208	12	US-10-434-599-2567
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206	12	US-10-435-114-41777
328	12	US-10-435-114-39488
151	16	US-10-220-120-265
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197	15	US-10-374-7686A-104
201	12	US-10-235-056A-110

16	495	28.3
17	495	27.3
18	476.5	28.3
19	476.5	27.3
20	476.5	27.3
21	350	20.0
22	288	16.5
23	288	16.5
24	288	16.5
25	199.5	11.4
26	191.5	11.0
27	191.5	11.0
28	191.5	11.0
29	191.5	11.0
30	191.5	11.0
31	191.5	11.0
32	191.5	11.0
33	189.5	10.8
34	189.5	10.8
35	189.5	10.8
36	189.5	10.8
37	189.5	10.8
38	187.5	10.7
39	187.5	10.7
40	187.5	10.7
41	183	10.5
42	183	10.5
43	181.5	10.4
44	178.5	10.2
45	178.5	10.2

ALIGNMENTS

```

RESULT 1
US-10-028-415-40
; Sequence 40, Application US/10028415
; Publication No. US20020151063A1
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Methods for Modulating Apoptotic Cell
; TITLE OF INVENTION: Death
; TITLE OF INVENTION: Death
; FILE REFERENCE: 11000.1004c3
; CURRENT APPLICATION NUMBER: US/10/028,415
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/NZ01/00286
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 09/724,809
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/036,004
; PRIOR FILING DATE: 1998-03-04
; PRIOR APPLICATION NUMBER: US 08/713,557
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Human
US-10-028-415-40

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Query Match	100.0%	Score 1747;	DB 13;	Length 324;
Best Local Similarity	100.0%;	Pred. No. 9.5e-127;		
Matches 324;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSSEAEQCPAAPPAAPALUSADTTKGGTTGSGAGSGGGGLTSAAPAGGDKVIATKVL	60	
Db	1	MSSEAEQCPAAPPAAPALUSADTTKGGTTGSGAGSGGGGLTSAAPAGGDKVIATKVL	60	
Qy	61	GTVKWFNVNRNGYGINENDTKEDVVFHQTAKKNPNPKYLRSGDGETVFEDVVEGEKGA	120	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1747	100.0	324	13	US-10-028-415-40	Sequence 40, Appl
2	1707	97.7	322	12	US-10-388-215-57	Sequence 57, Appl
3	1701	97.4	322	12	US-10-388-215-56	Sequence 56, Appl
4	1699	97.3	322	12	US-10-388-215-2	Sequence 2, Appl
5	1699	97.3	322	12	US-10-388-215-51	Sequence 51, Appl
6	1699	97.3	322	12	US-10-388-215-53	Sequence 53, Appl
7	1690	96.7	322	12	US-10-388-215-55	Sequence 55, Appl
8	1688	96.6	322	12	US-10-388-215-58	Sequence 58, Appl
9	1687	96.6	317	9	US-09-972-431-1	Sequence 1, Appl
10	1687	96.6	317	12	US-10-388-215-4	Sequence 4, Appl
11	1687	96.6	317	14	US-10-033-969-3	Sequence 3, Appl
12	773	44.2	412	15	US-10-440-464-124	Sequence 124, Appl
13	750.5	43.0	303	16	US-10-408-765A-1896	Sequence 1896, Ap
14	731	41.8	272	9	US-09-925-300-1697	Sequence 1697, Ap
15	640	36.6	64	12	US-10-434-599-280985	Sequence 280985,

Db 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 120
 QY 121 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRYNQYQNSGEGKESAPEG 180
 Db 121 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRYNQYQNSGEGKESAPEG 180
 QY 181 QAQRRPYRRRRFPYVYMRPPYGRPPQYNSPPVQGVMEGADNOGAGEQGRPVQNMRYG 240
 Db 181 QAQRRPYRRRRFPYVYMRPPYGRPPQYNSPPVQGVMEGADNOGAGEQGRPVQNMRYG 240
 QY 241 YRPRFRGPPRQRPREDGNEEDKENOGDETQGGPPQRRYRNFNRYRRRPNPKPDG 300
 Db 241 YRPRFRGPPRQRPREDGNEEDKENOGDETQGGPPQRRYRNFNRYRRRPNPKPDG 300
 QY 301 KETKAADPPAENSSAPEAQGGAE 324
 Db 301 KETKAADPPAENSSAPEAQGGAE 324

RESULT 2

US-10-388-215-57

; Sequence 57, Application US/10388215
 ; Publication No. US20030223975A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas K.
 ; APPLICANT: Fukada, Toshiyuki
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF PTP-1B
 ; FILE REFERENCE: 200125.440
 ; CURRENT APPLICATION NUMBER: US/10388,215
 ; CURRENT FILING DATE: 2003-03-11
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 57
 ; LENGTH: 322
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-388-215-57

Query Match 97.7%; Score 1707; DB 12; Length 322;
 Best Local Similarity 98.5%; Pred. No. 1.2e-123;
 Matches 319; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MSSEAEATQPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
 Db 1 MSSEAEATQPPAAP--AAALSAADTKPGSTGAGSGGPGGLTSAAPAGDKKVIATKVL 58
 QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 120
 Db 59 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 118
 QY 121 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRYNQYQNSGEGKESAPEG 180
 Db 119 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRYNQYQNSGEGKESAPEG 178
 QY 181 QAQRRPYRRRRFPYVYMRPPYGRPPQYNSPPVQGVMEGADNOGAGEQGRPVQNMRYG 240
 Db 179 QAQRRPYRRRRFPYVYMRPPYGRPPQYNSPPVQGVMEGADNOGAGEQGRPVQNMRYG 238
 QY 241 YRPRFRGPPRQRPREDGNEEDKENOGDETQGGPPQRRYRNFNRYRRRPNPKPDG 300
 Db 239 YRPRFRGPPRQRPREDGNEEDKENOGDETQGGPPQRRYRNFNRYRRRPNPKPDG 298
 QY 301 KETKAADPPAENSSAPEAQGGAE 324
 Db 299 KETKAADPPAENSSAPEAQGGAE 322

RESULT 3

US-10-388-215-56

; Sequence 56, Application US/10388215
 ; Publication No. US20030223975A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas K.

; APPLICANT: Fukada, Toshiyuki
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF PTP-1B
 ; FILE REFERENCE: 200125.440
 ; CURRENT APPLICATION NUMBER: US/10388,215
 ; CURRENT FILING DATE: 2003-03-11
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 56
 ; LENGTH: 322
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-388-215-56

Query Match 97.4%; Score 1701; DB 12; Length 322;
 Best Local Similarity 98.1%; Pred. No. 3.3e-123;
 Matches 318; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 MSSEAEATQPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
 Db 1 MSSEAEATQPPAAP--AAALSAADTKPGSTGAGSGGPGGLTSAAPAGDKKVIATKVL 58
 QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 120
 Db 59 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 118
 QY 121 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRYNQYQNSGEGKESAPEG 180
 Db 119 EAAVNTGGVPGVQGSKYAADRNHYRRYPRRRGPPRYNQYQNSGEGKESAPEG 178
 QY 181 QAQRRPYRRRRFPYVYMRPPYGRPPQYNSPPVQGVMEGADNOGAGEQGRPVQNMRYG 240
 Db 179 QAQRRPYRRRRFPYVYMRPPYGRPPQYNSPPVQGVMEGADNOGAGEQGRPVQNMRYG 238
 QY 241 YRPRFRGPPRQRPREDGNEEDKENOGDETQGGPPQRRYRNFNRYRRRPNPKPDG 300
 Db 239 YRPRFRGPPRQRPREDGNEEDKENOGDETQGGPPQRRYRNFNRYRRRPNPKPDG 298
 QY 301 KETKAADPPAENSSAPEAQGGAE 324
 Db 299 KETKAADPPAENSSAPEAQGGAE 322

RESULT 4

US-10-388-215-2

; Sequence 2, Application US/10388215
 ; Publication No. US20030223975A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas K.
 ; APPLICANT: Fukada, Toshiyuki
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF PTP-1B
 ; FILE REFERENCE: 200125.440
 ; CURRENT APPLICATION NUMBER: US/10388,215
 ; CURRENT FILING DATE: 2003-03-11
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 322
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-388-215-2

Query Match 97.3%; Score 1699; DB 12; Length 322;
 Best Local Similarity 98.1%; Pred. No. 4.8e-123;
 Matches 318; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 MSSEAEATQPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
 Db 1 MSSEAEATQPPAAP--AAALSAADTKPGSTGAGSGGPGGLTSAAPAGDKKVIATKVL 58
 QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 120
 Db 59 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 118

QY 121 EAANVTGPGVPOGSKYAADRNHYRRYPRRGGPPRNYQOYQNSSEGEKNEGSAPG 180
DB 119 EAANVTGPGVPOGSKYAADRNHYRRYPRRGGPPRNYQOYQNSSEGEKNEGSAPG 178
QY 181 QAQORRPPYRRRFPYMYRRPYARRPQYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 240
DB 179 QAQORRPPYRRRFPYMYRRPYARRPQYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 238
QY 241 YRPRFRGGPPRQORPREDNEEDKENOGDETQGOQPPORRYRRNFYRRRRPENPKPDG 300
DB 239 YRPRFRGGPPRQORPREDNEEDKENOGDETQGOQPPORRYRRNFYRRRRPENPKPDG 298
QY 301 KETKAADPPAENSSAPEAQGGAE 324
DB 299 KETKAADSPAENSSAPEAQGGAE 322

RESULT 5

US-10-388-215-51
; Sequence 51, Application US/10388215
; Publication No. US20030223975A1
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF PTP-1B
; FILE REFERENCE: 200125.440
; CURRENT APPLICATION NUMBER: US/10/388,215
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-388-215-51

Query Match 97.3%; Score 1699; DB 12; Length 322;
Best Local Similarity 98.1%; Pred. No. 4.8e-123;
Matches 318; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 MSSEAEATQPPAAPALSAADTKPGTTCGSGAGSGPGGLTSAAPAGGDKKVIATKVL 60
DB 1 MSSEAEATQPPAAP--AAALSAADTKPGTTCGSGAGSGPGGLTSAAPAGGDKKVIATKVL 58
QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLRSLVSGDGETVFDDVVEGEKGA 120
DB 59 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLRSLVSGDGETVFDDVVEGEKGA 118
QY 121 EAANVTGPGVPOGSKYAADRNHYRRYPRRGGPPRNYQOYQNSSEGEKNEGSAPG 180
DB 119 EAANVTGPGVPOGSKYAADRNHYRRYPRRGGPPRNYQOYQNSSEGEKNEGSAPG 178
QY 181 QAQORRPPYRRRFPYMYRRPYARRPQYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 240
DB 179 QAQORRPPYRRRFPYMYRRPYARRPQYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 238
QY 241 YRPRFRGGPPRQORPREDNEEDKENOGDETQGOQPPORRYRRNFYRRRRPENPKPDG 300
DB 239 YRPRFRGGPPRQORPREDNEEDKENOGDETQGOQPPORRYRRNFYRRRRPENPKPDG 298
QY 301 KETKAADPPAENSSAPEAQGGAE 324
DB 299 KETKAADSPAENSSAPEAQGGAE 322

RESULT 6

US-10-388-215-53
; Sequence 53, Application US/10388215
; Publication No. US20030223975A1
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF PTP-1B

; FILE REFERENCE: 200125.440
; CURRENT APPLICATION NUMBER: US/10/388,215
; CURRENT FILING DATE: 2003-03-11
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-388-215-53

Query Match 97.3%; Score 1699; DB 12; Length 322;
Best Local Similarity 98.1%; Pred. No. 4.8e-123;
Matches 318; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 MSSEAEATQPPAAPALSAADTKPGTTCGSGAGSGPGGLTSAAPAGGDKKVIATKVL 60
DB 1 MSSEAEATQPPAAP--AAALSAADTKPGTTCGSGAGSGPGGLTSAAPAGGDKKVIATKVL 58
QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLRSLVSGDGETVFDDVVEGEKGA 120
DB 59 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLRSLVSGDGETVFDDVVEGEKGA 118
QY 121 EAANVTGPGVPOGSKYAADRNHYRRYPRRGGPPRNYQOYQNSSEGEKNEGSAPG 180
DB 119 EAANVTGPGVPOGSKYAADRNHYRRYPRRGGPPRNYQOYQNSSEGEKNEGSAPG 178
QY 181 QAQORRPPYRRRFPYMYRRPYARRPQYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 240
DB 179 QAQORRPPYRRRFPYMYRRPYARRPQYSNPPVQGEVMEGADNQGAGEQGRPVQNNMYRG 238
QY 241 YRPRFRGGPPRQORPREDNEEDKENOGDETQGOQPPORRYRRNFYRRRRPENPKPDG 300
DB 239 YRPRFRGGPPRQORPREDNEEDKENOGDETQGOQPPORRYRRNFYRRRRPENPKPDG 298
QY 301 KETKAADPPAENSSAPEAQGGAE 324
DB 299 KETKAADSPAENSSAPEAQGGAE 322

RESULT 7

US-10-388-215-55
; Sequence 55, Application US/10388215
; Publication No. US20030223975A1
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF PTP-1B
; FILE REFERENCE: 200125.440
; CURRENT APPLICATION NUMBER: US/10/388,215
; CURRENT FILING DATE: 2003-03-11
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-388-215-55

Query Match 96.7%; Score 1690; DB 12; Length 322;
Best Local Similarity 97.8%; Pred. No. 2.4e-122;
Matches 317; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 MSSEAEATQPPAAPALSAADTKPGTTCGSGAGSGPGGLTSAAPAGGDKKVIATKVL 60
DB 1 MSSEAEATQPPAAP--AAALSAADTKPGTTCGSGAGSGPGGLTSAAPAGGDKKVIATKVL 58
QY 61 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLRSLVSGDGETVFDDVVEGEKGA 120
DB 59 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLRSLVSGDGETVFDDVVEGEKGA 118
QY 121 EAANVTGPGVPOGSKYAADRNHYRRYPRRGGPPRNYQOYQNSSEGEKNEGSAPG 180

Db	121	EAANYTGGGVFGQSKYAADNNHYRRYPYRRRPPRYNQYNSSESGKNEGSAPEG	180
Qy	181	QAQQRPPYRRRRFPYVYRRYPYGRRPPOYSNPVQGEVMEGADNQAGEQGRFVRQNMVYRG	240
Db	181	QAQQRPPYRRRRFPYVYRRYPYGRRPPOYSNPVQGEVMEGADNQAGEQGRFVRQNMVYRG	240
Qy	241	YPRFRPPPPRQRPREDNGNEEDKENQGDGTQGGQPPORRYRNFYRRRRRPPENPKPDG	300
Db	241	YPRFRPPPPRQRPREDNGNEEDKENQGDGTQGGQPPORRYRNFYRRRRRPPENPKPDG	300
Qy	301	KETKAADPPAENS 313	
Db	301	KETKAADPPAENS 313	

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RESULT 11
US-10-023-969-3
; Sequence 3, Application US/10023969
; Publication NO. US20030095989A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Irving John
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Chimeric Cytolytic Viruses for Cancer Treatment
; FILE REFERENCE: 084,002
; CURRENT APPLICATION NUMBER: US/10/023,969
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/256,418
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ.ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-969-3

```

[illegible]

RESULT 12
US-10-440-464-124
; Sequence 124, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL

```

; APPLICANT: O' FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 124
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-124

Query Match          44.2%; Score 773; DB 15; Length 412;
Best Local Similarity 52.1%; Pred. No. 1.8e-51;
Matches 185; Conservative 24; Mismatches 72; Indels 74; Gaps 15;

Qy      1  MSEA-----TQPPAAPAAALSNADTKP-GTTGSGAG-----SSGPGGLT 43
Db      71  MSEAAGEATTTTTTLPOAPTEAAAAAPQDPAPKSPVGSAPQAAAPAAAHVAGNPGG-- 129

Qy      44  SAAPAG-----GDKKVIATKVLGTWKFNVRNGYGFINRNDTKEDV 86
Db      129  DAFAATGTAASLAASLAAGSDEAKKVLATKVLGTWKFNVRNGYGFINRNDTKEDV 188

Qy      87  HQTAIKKNPKYLSRSGDGETVEFDVVEGKGAEAANVTGPGGVPVQGSKYAADRNHYR 146
Db      189  HQTAIKKNPKYLSRSGDGETVEFDVVEGKGAEAANVTGPDGVPVEGSRYAADRRYR 248

Qy      147  R--YPRRGGRPNYQNYQNSGEKNGESGAPEG-----QAQQRPP----- 187
Db      249  RGYVGRGRGPRPNY-----AGEEEEGSGSGEFPDPATDRQFSGARNQLRRPQYRP 300

Qy      188  -YRRRRPPPYMRRPYGRRPQ---YSNPVPVQGEVWEGADN--QGAGGQGRPVQNMYRGY 241
Db      301  QYRQRPPPTHVGGTDRERSVLPHPNRIQAGEIGEMKDGYPEGAQLQG-PVHEN--PTY 357

Qy      242  RPFR-RGPRRQRFREDGNEEDKENOGDETQGOQPPQRR-YRRNFYRNRPRPN 294
Db      358  RPYRYSRGPRPRPAPAVGAEDKENQOATSGNPQSVRRGYRRPYNRRPPSS 412

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RESULT 13
US-10-408-765A-1896
; Sequence 1896, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fathy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408.765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077

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; SOFTWARE: FastSeq for Windows-Version 4.0
; SEQ ID NO 1896
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1896

Query Match      43.0%; Score 750.5; DB 16; Length 303;
Best Local Similarity 49.9%; Pred. No. 6.9e-50;
Matches 181; Conservative 15; Mismatches 68; Indels 99; Gaps 14;

QY 1 MSSEAE-----TOOPPAAPPAAPALSAADTKP-CTTGSAG-----SGPGGLT 43
Db 1 MSEAGEATTTTTLPCAPTEAAAAAQQDPAPKSPVSGAPAAAPAAHVAGNFGG-- 58
QY 44 SAAPAG-----GDKVIATKVLGTVKFNVRNGYGFINRNDTKEDVFV 86
Db 59 DAAPAAATGTAATAAAGSDEAEKKVLATKVLGTVKFNVRNGYGFINRNDTKEDVFV 118
QY 87 HTAIKKNPKYLSVGDGETVEFVVEGEGKGAEEAANTGPGVPVQGSKYAADRNHYR 146
Db 119 HTAIKKNPKYLSVGDGETVEFVVEGEGKGAEEAANTGPGVPVQGSKYAADRNHYR 178
QY 147 R--YPRRGPRNTYQNYQNSSEKNEGSESAPEGAQQRRPYRRRRFPYTYRRPYGR 204
Db 179 RGYGRRRRGPRN-----AGEIGEMKDGVPPEG-AQLQGPVHR----- 214
QY 205 RPQYSNPVQGVVEGADNQGAGEQGRPVQNMVRYRPRFR-RGPRQRPREDGNEED 263
Db 215 -----NPT-----YRPRYRSGPRPRPAPVAGEAD 241
QY 264 KENQDETQGGQPPQRR-YRRNFNYYRR-RPENPKQDGKHTKAADPPAENSAPAEQG 321
Db 242 KENQATSGNPQSVRGYRRPYRRRPPNPPNAPSQDGKEAKAGEAPTEN-PAPTQQS 300
QY 322 GAE 324
Db 301 SAE 303

RESULT 14
US-09-925-300-1697
; Sequence 1697, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Ruben,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1897
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (256)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (258)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (262)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (263)
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1697

Query Match      41.8%; Score 731; DB 9; Length 272;
Best Local Similarity 53.5%; Pred. No. 1.9e-48;
Matches 166; Conservative 15; Mismatches 59; Indels 70; Gaps 10;

QY 17 APALSA-----DTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVLGTVKFNVRNG 71
Db 2 APAAHVAGNPGGDAAPAAATGTAAAA---SLATAAGSEDAEKKVLATKVLGTVKFNVRNG 58
QY 72 YGFINRNDTKEDVFVHTAIKKNPKYLSVGDGETVEFVVEGEGKGAEEAANTGPGGV 131
Db 59 YGFINRNDTKEDVFVHTAIKKNPKYLSVGDGETVEFVVEGEGKGAEEAANTGPDGV 118
QY 132 PVQGSKYAADRNHYR--YPRRGPRNTYQNYQNSSEKNEGSESAPEGAQQRRPYR 189
Db 119 PVESRYAADRRRYRARGYGRRRGPPN-----AGEIGEMKDGVPPEG-AQLQGPVH 168
QY 190 RRRFPFYNNRRPYRRRPOYSNPPVQGVVEGADNQGAGEQGRPVQNMVRYRPRFR-RG 248
Db 169 R-----NPT-----YRPRYRSG 181
QY 249 PPRQRPREDGNEEDKENQDETQGGQPPQRR-YRRNFNYYRR-RPENPKQDGKHTKAA 306
Db 182 PRRPRPAPVAGEADKENQATSGNPQSVRGYRRPYRRRPPNPPNAPSQDGKEAKAG 241
QY 307 DPPAENSAP 316
Db 242 EAPTENPAPP 251

RESULT 15
US-10-424-599-280985
; Sequence 280985, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 280985
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95751C.1.pap
US-10-424-599-280985

Query Match      36.6%; Score 640; DB 12; Length 164;
Best Local Similarity 99.2%; Pred. No. 1.1e-41;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSSEAEETQOPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVL 60
Db 41 MSSEAEETQOPPAAPVAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVL 100
QY 61 GTVKNFVRNGYGFINRNDTKEDVFVHTAIKKNPKYLSVGDGETVEFVVEGEGKGA 120
Db 101 GTVKNFVRNGYGFINRNDTKEDVFVHTAIKKNPKYLSVGDGETVEFVVEGEGKGA 160
QY 121 EAA 124
Db 161 EAA 164
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Search completed: August 25, 2004, 00:38:03
Job time : 129 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OX protein - protein search, using sw model
Run on: August 25, 2004, 00:18:50 ; Search time 40 Seconds
(without alignments)
779.151 Million cell updates/sec
Title: US-10-028-415-40
Perfect score: 1747
Sequence: 1 MSSEATQPPAAPPAAL.....AADPPAENSAPAEQGGAE 324
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1747	100.0	324	1 I39382	y box-binding prot
2	1747	100.0	324	1 J0292	y box-binding prot
3	1728	98.9	324	1 A55971	y box-binding prot
4	1701	97.4	322	1 I58195	y box-binding prot
5	1699	97.3	322	1 A23677	y box-binding prot
6	1589.5	91.0	321	1 A48136	nuclease sensitive
7	1383	79.2	321	1 S34426	y box-binding prot
8	1350.5	77.3	303	1 A38274	y box-binding prot
9	1304.5	74.7	305	1 S22313	B box-binding prot
10	1246	71.3	348	2 A49594	enhancer factor pr
11	840	48.1	372	2 S69501	DNA-binding protei
12	773	44.2	342	1 I53354	DNA-binding protei
13	742.5	42.5	291	2 S51608	RYB-a protein - ra
14	742.5	42.5	291	2 S48055	RYB-a protein - ra
15	633	36.2	336	1 B38274	y box-binding prot
16	606.5	34.7	324	1 A41766	mRNA-binding prote
17	461	26.4	140	4 J02293	transcription enha
18	435	24.9	178	2 JC2032	enhancer factor I
19	393	22.5	208	2 T21689	hypothetical prote
20	316.5	18.1	294	2 T19920	hypothetical prote
21	281	16.1	74	2 S62829	y-box binding prot
22	281	16.1	267	2 T25767	hypothetical prote
23	265.5	15.2	265	2 T29322	hypothetical prote
24	200.5	11.5	83	2 JC2021	enhancer factor I
25	186.5	10.7	214	1 KNT05	glycine-rich prote
26	178.5	10.2	201	2 P84536	glycine-rich prote
27	172	9.8	69	2 A84987	cold shock-like pr
28	170.5	9.8	66	2 A89853	cold-shock protein
29	169	9.7	69	2 AH0579	cold shock-like pr

30	168.5	9.6	65	2 B84101	cold-shock protein
31	168.5	9.6	203	1 JQ1061	glycine-rich prote
32	166.5	9.5	65	2 H97267	cold shock protein
33	164	9.4	69	2 S49050	cold shock protein
34	164	9.4	69	2 AG0316	probable cold shoc
35	164	9.4	69	2 A10212	cold shock protein
36	164	9.4	69	2 B85562	cold shock protein
37	164	9.4	69	2 F90711	cold shock protein
38	164	9.4	70	2 D64840	cold shock protein
39	164	9.4	70	2 A30772	cold shock-like pr
40	164	9.4	70	2 E85634	homolog of Salmone
41	163	9.3	69	2 S43618	cold shock protein
42	163	9.3	69	2 E90945	cold shock protein
43	163	9.3	69	2 A80727	cold shock-like pr
44	163	9.3	69	2 H85793	cold shock protein
45	161.5	9.2	66	2 AF1681	cold shock protein

ALIGNMENTS

RESULT 1
I39382
Y box-binding protein 1 - human
N:Alternate names: DNA binding protein B; transcription enhancer factor EF1a; transcrip
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1998 #sequence revision 16-Feb-1996 #text_change 22-Jun-1999
C:Accession: I39382; PS0015; A40498
R:Horwitz, E.M.; Maloney, K.A.; Lev, T.J.
J. Biol. Chem. 269, 14130-14139, 1994
A:Title: A human protein containing a 'cold shock' domain binds specifically to H-DNA u
A:Reference number: A54085; MUID:94245734; PMID:8188694
A:Accession: I39382
A:Molecule type: mRNA
A:Residues: 1-324 <RES>
A:Cross-references: GB:L28809; NID:9454151; PIDN:AAA20871.1; PID:9454152
R:Sakura, H.; Maekawa, T.; Imamoto, F.; Yasuda, K.; Ishii, S.
Gene 73, 499-507, 1988
A:Title: Two human genes isolated by a novel method encode DNA-binding proteins contain
A:Reference number: PS0014; MUID:89211987; PMID:2977358
A:Accession: PS0015
A:Molecule type: mRNA
A:Residues: 'EFGQPRALSSPTAAGLVITPREPQLPQAPVITAT', 1-324 <SAK>
A:Cross-references: GB:M24070; NID:G181485; PIDN:AAA35750.1; PID:G181486
R:Didier, D.K.; Schifffenbauer, J.; Woulfe, S.L.; Zacheis, M.; Schwartz, B.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7322-7326, 1988
A:Title: Characterization of the cDNA encoding a protein binding to the major histocomp
A:Reference number: A40498; MUID:89017190; PMID:3174636
A:Accession: A40498
A:Molecule type: mRNA
A:Residues: 1-119, 'E', 121-313, 'RSRG' <DID>
A:Cross-references: GB:J03827; NID:G340418; PIDN:AAA61308.1; PID:G340419
C:Genetics:
A:Gene: GDB:YB1
A:Cross-references: GDB:5577123; OMIM:154030.
A:Map position: lp34-1p34
C:Superfamily: Y box-binding protein 1; cold shock domain homology
C:Keywords: DNA binding; nucleus; transcription regulation
F:61-125/Domain: cold shock domain homology <CSD>

Query Match	100.0%	Score	1747;	DB	1;	Length	324;
Best Local Similarity	100.0%	Pred. No.	4.6e-99;				
Matches	324;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MSSEATQPPAAPPAALSAADTKPGTTSAGSGGPGGLTSAAPAGGDKKVIATKVL	60				
Db	1	MSSEATQPPAAPPAALSAADTKPGTTSAGSGGPGGLTSAAPAGGDKKVIATKVL	60				
QY	61	GVTKWPNVNGYGFNRNDTKEDVFVHQTAKNNPRKYLRSVGGETVFVWVEGEKA	120				
Db	61	GVTKWPNVNGYGFNRNDTKEDVFVHQTAKNNPRKYLRSVGGETVFVWVEGEKA	120				
QY	121	EAANTGPGGVFQGSKYAADRNHYRRYPRRRPPRRYQNYQNSGESGKNGESSAPEG	180				

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Db 121 EAAVNTGGVPGVGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEGKESGSAPEG 180
Qy 181 QAQORRRYRRRRFPYMYRRPGRPOYSNPPVQGVWEGADNQAGEQGRPVQRQNYRG 240
Db 181 QAQORRRYRRRRFPYMYRRPGRPOYSNPPVQGVWEGADNQAGEQGRPVQRQNYRG 240
Qy 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNRRPNPKPDG 300
Db 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNRRPNPKPDG 300
Qy 301 KETKAADPPAENSAPAEQGGAE 324
Db 301 KETKAADPPAENSAPAEQGGAE 324

RESULT 2
QJ2292
Y box-binding protein 1 - bovine
N:Alternate names: DNA binding protein B; transcription enhancer factor Bf1a; transcrip
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 22-Jun-1999
C:Accession: JQ2292
R:Ozer, J.; Chalkley, R.; Sealy, L.
Gene 124, 223-230, 1993
A:Title: Isolation of the CCAAT transcription factor subunit EF1A cDNA and a potentia
amly.
A:Reference number: JQ2292; MUID:93185927; PMID:8444345
A:Accession: JQ2292
A:Molecule type: mRNA
A:Residues: 1-324 <OE>
A:Cross-references: GB:M95793; NID:g162982; PIDN:AAA30497.1; PID:g162983
C:Comment: This protein is a multi-subunit trans-acting complex that binds to CCAAT box
C:Superfamily: Y box-binding protein 1; cold shock domain homology
C:Keywords: DNA binding; nucleus; transcription regulation
F:61-125/Domain: cold shock domain homology <CSD>

Query Match 100.0%; Score 1747; DB 1; Length 324;
Best Local Similarity 100.0%; Pred. No. 4.6e-99;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSEAEQQPPAAPALSAADTKPGTTGSGAGSGPGGLTSAAPAGDKKVIATKVL 60
Db 1 MSSEAEQQPPAAPALSAADTKPGTTGSGAGSGPGGLTSAAPAGDKKVIATKVL 60
Qy 61 GTVKWFWNRNGYGFNRNDTKEDVFVHQTAKNNPKYLSVGDGETVEFDVVEGEKA 120
Db 61 GTVKWFWNRNGYGFNRNDTKEDVFVHQTAKNNPKYLSVGDGETVEFDVVEGEKA 120
Qy 121 EAAVNTGGVPGVGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEGKESGSAPEG 180
Db 121 EAAVNTGGVPGVGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEGKESGSAPEG 180
Qy 181 QAQORRRYRRRRFPYMYRRPGRPOYSNPPVQGVWEGADNQAGEQGRPVQRQNYRG 240
Db 181 QAQORRRYRRRRFPYMYRRPGRPOYSNPPVQGVWEGADNQAGEQGRPVQRQNYRG 240
Qy 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNRRPNPKPDG 300
Db 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNRRPNPKPDG 300
Qy 301 KETKAADPPAENSAPAEQGGAE 324
Db 301 KETKAADPPAENSAPAEQGGAE 324

RESULT 3
A55971
Y box-binding protein 1 - rabbit
N:Alternate names: DNA binding protein B; transcription enhancer factor Bf1a; transcrip
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C:Accession: A55971

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R:Evdokimova, V.M.; Wei, C.L.; Sitikov, A.S.; Simonenko, P.N.; Lazarev, O.A.; Vasilenko,
J. Biol. Chem. 270, 3186-3192, 1995
A:Title: The major protein of messenger ribonucleoprotein particles in somatic cells is
A:Reference number: A55971; MUID:95155408; PMID:7852402
A:Accession: A55971
A:Molecule type: mRNA
A:Residues: 1-324 <EVD>
A:Cross-references: GB:U16821; NID:g608517; PIDN:AAA6069.1; PID:g608518
C:Superfamily: Y box-binding protein 1; cold shock domain homology
C:Keywords: DNA binding; phosphoprotein; RNA binding; transcription regulation; translat
F:61-125/Domain: cold shock domain homology <CSD>

Query Match 98.9%; Score 1728; DB 1; Length 324;
Best Local Similarity 98.8%; Pred. No. 6.5e-98;
Matches 320; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSSEAEQQPPAAPALSAADTKPGTTGSGAGSGPGGLTSAAPAGDKKVIATKVL 60
Db 1 MSSEAEQQPPAAPALSAADTKPGTTGSGAGSGPGGLTSAAPAGDKKVIATKVL 60
Qy 61 GTVKWFWNRNGYGFNRNDTKEDVFVHQTAKNNPKYLSVGDGETVEFDVVEGEKA 120
Db 61 GTVKWFWNRNGYGFNRNDTKEDVFVHQTAKNNPKYLSVGDGETVEFDVVEGEKA 120
Qy 121 EAAVNTGGVPGVGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEGKESGSAPEG 180
Db 121 EAAVNTGGVPGVGSKYAADRNHYRRYPRRRGPPRYQNYQNSGEGKESGSAPEG 180
Qy 181 QAQORRRYRRRRFPYMYRRPGRPOYSNPPVQGVWEGADNQAGEQGRPVQRQNYRG 240
Db 181 QAQORRRYRRRRFPYMYRRPGRPOYSNPPVQGVWEGADNQAGEQGRPVQRQNYRG 240
Qy 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNRRPNPKPDG 300
Db 241 YRPRFRGPPRQRPREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNRRPNPKPDG 300
Qy 301 KETKAADPPAENSAPAEQGGAE 324
Db 301 KETKAADPPAENSAPAEQGGAE 324

RESULT 4
I58195
Y box-binding protein 1 - mouse
N:Alternate names: DNA binding protein B; MSY1 protein; transcription enhancer factor EF
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
C:Accession: I58195; A45976; I52910; S22822
R:Wolffe, A.P.; Taruri, S.; Ranjan, M.; Familari, M.
New Biol. 4, 290-298, 1992
A:Title: The Y-box factors: a family of nucleic acid binding proteins conserved from Esc
A:Reference number: I58195; MUID:92322631; PMID:1622927
A:Accession: I58195
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-322 <RBS>
A:Cross-references: GB:M62867; NID:g199820; PIDN:AAA63390.1; PID:g199821
R:Tatari, S.R.; Familari, M.; Wolffe, A.P.
J. Biol. Chem. 268, 12213-12220, 1993
A:Title: A mouse Y box protein, MSY1, is associated with paternal mRNA in spermatocytes.
A:Reference number: A45976; MUID:93280200; PMID:8505341
A:Accession: A45976
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-322 <TAR>
R:Shaughnessy, M.; Lee, D.; Wistow, G.J.
Curr. Eye Res. 11, 171-181, 1992
A:Title: Absence of MHC expression in lens and cloning of dbpB/YB-1, a DNA-binding prote
A:Reference number: I52910
A:Accession: I52910
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-28,'G',30-322 <RE2>

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A:Cross-references: GB:M60419; NID:g202434; PIDN:AAA40577.1; PID:g202435
A:Experimental source: lens
R:Gal, X.; Lipson, K.E.; Prystowsky, M.B.
Nucleic Acids Res. 20, 601-606, 1992
A:Title: Unusual DNA binding characteristics of an in vitro translation product of the C
A:Reference number: S22822; MUID:92158671; PMID:1741293
A:Accession: S22822
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: mRNA
A:Residues: 1-28, 'G', '30-42', 'RR', '46-237', 'P', '239-322 <GAI>
A:Cross-references: EMBL:X57621; NID:g95450; PIDN:CAA40847.1; PID:g55451
A:Experimental source: strain C57BL/6
C:Genetics:
A:Gene: MSY-1; YB-1
C:Superfamily: Y box-binding protein 1; cold shock domain homology
C:Keywords: DNA binding; eye lens; nucleus; RNA binding; testis; transcription regulation
F:59-123/Domain: cold shock domain homology <CSD>

Query Match 97.4%; Score 1701; DB 1; Length 322;
Best Local Similarity 98.1%; Pred. No. 2.8e-96;
Matches 318; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 MSSEATQPPAAPALPSAADTKPGTTGSGAGSGPGGLTSAAPAGGDKKIATKVL 60
Db 1 MSSEATQPPAAP--AAALSAADTKPGSTAGSGSGPGGLTSAAPAGGDKKIATKVL 58
QY 61 GTVKKFNVRNGVGFINRNTDKEDVFHQTAIKKNPKYLSVGDGETVEFDDVEGEKGA 120
Db 59 GTVKKFNVRNGVGFINRNTDKEDVFHQTAIKKNPKYLSVGDGETVEFDDVEGEKGA 118
QY 121 EAANVTGPGVPVQGSKYAADRNHYRYPRRRPPPNYQNYQNSSEGEKNGSESAPBG 180
Db 119 EAANVTGPGVPVQGSKYAADRNHYRYPRRRPPPNYQNYQNSSEGEKNGSESAPBG 178
QY 181 QAOQRPYRRRPPPYMYRRPYGRRPOYNPNPVQGEVMGADNQGAGEGRPVQRNNYRG 240
Db 179 QAOQRPYRRRPPPYMYRRPYARRPOYNPNPVQGEVMGADNQGAGEGRPVQRNNYRG 238
QY 241 YRPFRRGPPRQRPREDGNEEDKENQGDQTCQCPQRRYRRNFYRRRRRPNKPDG 300
Db 239 YRPFRRGPPRQRPREDGNEEDKENQGDQTCQCPQRRYRRNFYRRRRRPNKPDG 298
QY 301 KETKAADPPAENSAPAEQGGAE 324
Db 299 KETKAADPPAENSAPAEQGGAE 322

RESULT 5
A23677

Y box-binding protein 1 - rat
N:Alternate names: DNA binding protein B; transcription enhancer factor Bfla; transcript
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Oct-1991 #sequence_revision 31-Jul-1992 #text_change 22-Jun-1999
C:Accession: A23677
R:Ozer, J.; Faber, M.; Chalkley, R.; Sealy, L.
J. Biol. Chem. 285, 22143-22152, 1990
A:Title: Isolation and characterization of a cDNA clone for the CCAAT transcription factor
A:Reference number: A23677; MUID:91093048; PMID:1967130
A:Accession: A23677
A:Molecule type: DNA
A:Residues: 1-322 <OZE>
A:Cross-references: GB:M57299; GB:J05704; NID:g203998; PIDN:AAA41108.1; PID:g203999
C:Superfamily: Y box-binding protein 1; cold shock domain homology
C:Keywords: DNA binding; nucleus; transcription regulation
F:59-123/Domain: cold shock domain homology <CSD>

Query Match 97.3%; Score 1699; DB 1; Length 322;
Best Local Similarity 98.1%; Pred. No. 3.7e-96;
Matches 318; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 MSSEATQPPAAPALPSAADTKPGTTGSGAGSGPGGLTSAAPAGGDKKIATKVL 60
Db 1 MSSEATQPPAAP--AAALSAADTKPGSTAGSGSGPGGLTSAAPAGGDKKIATKVL 58

Db 277 KPQGGKTKAETSAAETSAPEAEQGGAE 305

RESULT 10
A49594
enhancer factor protein 1 - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 20-Aug-1999
C/Accession: A49594
R:Kandala, J.C.; Guntaka, R.V.
Virolgy 198, 514-523, 1994
A>Title: Cloning of Rous sarcoma virus enhancer factor genes. I. Evidence that RSV-EF 1
A/Reference number: A49594; MUID:94120725; PMID:8291233
A/Accession: A49594
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-348 <KAN>
A/Cross-references: GB:L20500; NID:G304377; PIDN:AAA18017.1; PID:G304378
C:Superfamily: Y box-binding protein 1; cold shock domain homology
C/Keywords: DNA binding; nucleus
F:93-157/Domain: cold shock domain homology <CSD>

Query Match 71.3%; Score 1246; DB 2; Length 348;
Best Local Similarity 75.0%; Pred. No. 1.1e-68;
Matches 243; Conservative 15; Mismatches 48; Indels 18; Gaps 4;

QY 5 AETQCP-----PAAPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATK 58
DB 4 AETQPPAAPVPAPPPPTPNLTAA-----AGTAAAWRRRLRRGQGH-----RNE 52

QY 59 VLGTWKFNVRNGYGFNRNDTKEDVFVHTQAIKKNPRKYLRSVGDGTVEFDVVEGK 118
DB 53 GFGNSEMVNVRNGYGLMRNDTKEDVFVHTQAIKKNPRKYLRSVGDGTVEFDVVEGK 112

QY 119 GAERANVTGPGVQVQSKYAADNHYRRYRRPGRGPRNYYQONVQNSGSEKVEGESAP 178
DB 113 GAERANVTGPGVQVQSKYAADNHYRRYRRYRVAGVLHATTSTENSEGSEKKEGAENIP 172

QY 179 EGQAQRRPYRRRPPYRRPVRGRRPOKSNPNPQVEVMEGADNQGAGQGRRPVRQNM 238
DB 173 EGQAQRRPYRRRPPYRRPVRGRRPTG-RPOYSNAPVQGEIVGADNQGAGQGRRPVRQNM 231

QY 239 RGYRFRFRGPRGPRQRPREDNEDKENQDGTGQGPQRRYRNRYRRRPNPKPQ 298
DB 232 RGYRFRFRGPRGPRQRPREDNEDKENQDGTGQGPQRRYRNRYRRRPNPKPQ 291

QY 299 DGKETKAADPAENSSAPEAEQGG 322
DB 292 DGKETKAEPPEAETSAPAEQAG 315

RESULT 11
S69501
DNA-binding protein A variant - human
N/Alternate names: cold shock domain protein A
C:Species: Homo sapiens (man)
C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C/Accession: S69501
R:Coles, L.S.; Diamond, P.; Occhiodoro, F.; Vadas, M.A.; Shannon, M.F.
Nucleic Acids Res. 24, 2311-2317, 1996
A>Title: Cold shock domain proteins repress transcription from the GM-CSF promoter.
A/Reference number: S69501; MUID:96279731; PMID:8710501
A/Accession: S69501
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-372 <COL>
A/Cross-references: EMBL:X95325; NID:g1167837; PIDN:CAA64631.1; PID:g1167838
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
C:Superfamily: Y box-binding protein 1; cold shock domain homology
F:93-157/Domain: cold shock domain homology <CSD>

Query Match 48.1%; Score 840; DB 2; Length 372;
Best Local Similarity 52.3%; Pred. No. 4.6e-44;

Matches 202; Conservative 25; Mismatches 83; Indels 76; Gaps 17;

QY 1 MSSEAE-----TQPPPAAPPAALSAADTKP-GTTGSGAG-----SGGPGGLT 43
DB 1 MSEAGEATTTTTTTLFQAPTEAAAAAQQDPAPKPSVGSAGPQAAAPAAHVAHNPFG-- 58

QY 44 SAAPAG-----GDKVIATKVLGTGVKFNVRNGYGFNRNDTKEDVFV 86
DB 59 DAAPPAATGTAAAAASLATAAGSDAEKKVLATKVLGTGVKFNVRNGYGFNRNDTKEDVFV 118

QY 87 HQTATKKNPRKYLRSVGDGTVEPDVVEGKGAFAAANVTGPGVVOGSKYAADRNYR 146
DB 119 HQTATKKNPRKYLRSVGDGTVEPDVVEGKGAFAAANVTGPGVVEGSKYAADRNYR 178

QY 147 R--YRRRGPRNYYQONVQNSGSEKNGSESAPG-----QAQRRP----- 187
DB 179 RYVYRRRGPRNYY-----AGEEEEGSGSGGDFPDPATDROFSGARVQLRRPQYRP 230

QY 188 -YRRRRFPYRRYRRPGRPQ---YSNPPVQGEVMEGADN--QGAGEQGRPVRQNMRYG 241
DB 231 QYRQRFPYRVHVGQTFDRRRVLPHNRIQAGEIGEMKDGVPGEAQLQG--PVHRR--PTY 287

QY 242 RRRFR-RGPPRQRPREDNEDKENQDGTGQGPQRR-RYRNFNRYRR--RPNPKPQ 298
DB 288 RPYRFRGPRGPRPAPVAGEADKENQATSGNPSVRRGYRRYRPNYRRRPPNAPSQ 347

QY 299 DGKETKAADPAENSSAPEAEQGGAE 324
DB 348 DGKEAKAGEAPTEN-PAPPTQQSAAE 372

RESULT 12
I53354
DNA-binding protein A - human
C:Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2000
C/Accession: I53354; PS0014; S65945
R:Kudo, S.; Mattei, M.G.; Fukuda, M.
Eur. J. Biochem. 231, 72-82, 1995
A/Title: Characterization of the gene for dbpA, a family member of the nucleic-acid-binding protein A.
A/Reference number: I53354; MUID:95354705; PMID:7628487
A/Accession: I53354
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-342 <KUD>
A/Cross-references: GB:L29071; NID:G950337; PIDN:AAA79243.1; PID:G950340
A/Experimental source: placenta
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R:Sakura, H.; Maekawa, T.; Imamoto, F.; Yasuda, K.; Ishii, S.
Gene 75, 499-507, 1988
A/Title: Two human genes isolated by a novel method encode DNA-binding proteins contain
A/Reference number: PS0014; MUID:89211987; PMID:2977358
A/Accession: PS0014
A/Molecule type: mRNA
A/Residues: EFGRGSPRRARRSSRLRQDRPSTAAGLRRIIRPGLPESEPRPPPPAALTADQPPRRRLSESRRGGG', 1-
A/Cross-references: GB:M24069; NID:g181483; PIDN:AAA35749.1; PID:g181484
C/Genetics:
A/Gene: GDB:CSDA; dbpA
A/Cross-references: GDB:9865772; OMIM:603437
A/Map position: 12p13.1-12p13.1
A/Introns: 88/1; 109/2; 120/3; 150/3; 191/3; 260/3; 293/2
C:Superfamily: Y box-binding protein 1; cold shock domain homology
C/Keywords: DNA binding; nucleus; transcription regulation
F:93-157/Domain: cold shock domain homology <CSD>

Query Match 44.2%; Score 773; DB 1; Length 342;
Best Local Similarity 52.1%; Pred. No. 4.9e-40;
Matches 185; Conservative 24; Mismatches 72; Indels 74; Gaps 15;

QY 1 MSSEAE-----TQPPPAAPPAALSAADTKP-GTTGSGAG-----SGGPGGLT 43
DB 1 MSEAGEATTTTTTTLFQAPTEAAAAAQQDPAPKPSVGSAGPQAAAPAAHVAHNPFG-- 58

44 SAAPAG-----GDKVIATKVLGTGVKFNVRNGYGFINRNDTKEDVFV 86
 59 DAAPATGTAASALAAAGSEDAEKKVLAATKVLGTGVKFNVRNGYGFINRNDTKEDVFV 118
 87 HQTAKKNNPKYILRSVGDGETVFDVVEGKGAEEAANVTGPGVPGVQGSKYAADRNHYR 146
 119 HQTAKKNNPKYILRSVGDGETVFDVVEGKGAEEAANVTGPGVPGVQGSKYAADRNHYR 178
 147 R--YRRRGGPRNYQONTSEGEKNGSESAPG-----QAQORRP----- 187
 179 RGYRRGGPRNY-----AGEEEEGSGSGEDFPATDRQFSGARNQLRPPQYRP 230
 188 -YRRRPPYRRPYGRRPO---YSNPFGVQGVVEGADN---QAGBQGRPVQNNYRGY 241
 231 QYRQRFPYHVQTFDRSRVLFHPNRIOAGEIGEMKMGVPEGAQLQG-PVHFN--PTY 287
 242 RPRFR-RGPRRQRPREDGNEEDKENQDETQGOQPPQRR-YRNNFYRRRPPEN 294
 288 RPRYSRGGPRRPPAPAVGEADKENQATSGPNQPSVRRGYRRPYNRRRPPSS 342

RESULT 13
 S51608
 RYB-a protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Jun-2000
 C:Accession: S51608
 R:Rito, K.; Tsutsumi, K.I.; Kuzumaki, T.; Gomez, P.F.; Otsu, K.; Ishikawa, K.
 submitted to the EMBL Data Library, February 1994
 A:Reference number: S51608
 A:Accession: S51608
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-291 <I>
 A:Cross-references: EMBL:D28557; NID:G505133; PID:G505133
 C:Superfamily: Y box-binding protein 1; cold shock domain homology
 F:84-148/Domain: cold shock domain homology <CSD>

Query Match 42.5%; Score 742.5; DB 2; Length 291;
 Best Local Similarity 51.0%; Pred. No. 2.9e-38;
 Matches 171; Conservative 16; Mismatches 75; Indels 73; Gaps 9;
 2 SSEATQPPAAPPAALSAADTKPGTTGSGAGS-----GGPGGLTSAAPAGDKKV 54
 18 AADAPAAAPDPAPKSPAAAGAPAPAPALLAGAPARRSPRAPGLISPRGKREKKV 77
 55 IATKVLGTGVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYILRSVGDGETVFDV 114
 78 LATKVLGTGVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYILRSVGDGETVFDV 137
 115 EGEKGAEEAANVTGPGVPGVQGSKYAADRNHYR--YRRRGGPRNYQONTSEGEKNE 172
 138 EGEKGAEEAANVTGPGVPGVQGSKYAADRNHYR--YRRRGGPRNYQONTSEGEKNE 188
 173 GSEAPG-QAQRPPYRRRPPYRRPYGRRPQYNSNPPVQGVVEGADNQAGEOGR 231
 189 MKDGVPEGAQLQVHR-----NPT----- 206
 232 PVQNNYRGYRRFRFRGPPRQRPREDGNEEDKENQDETQGOQPPQRR-YRNNFYRRR 290
 207 -----YRFRFRGPPRPPAPALGEADKENQAANGPNQPSARRGFRFPYNYRR 257
 291 -RPNPKPDGKTKAADPPAENSSAPEAQGGAE 324
 258 PRPLNAVSDGKETKAGEAPTEN-PAPATEQSSAE 291

RESULT 14
 S48055
 RYB-a protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 26-Feb-1998
 C:Accession: S48055

R:Ito, K.; Tsutsumi, K.; Kuzumaki, T.; Gomez, P.F.; Otsu, K.; Ishikawa, K.
 Nucleic Acids Res. 22, 2036-2041, 1994
 A:Title: A novel growth-inducible gene that encodes a protein with a conserved cold-shoc
 A:Reference number: S48055; MUID:94301785; PMID:8029009
 A:Accession: S48055
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-291 <I>
 A:Cross-references: EMBL:D28557
 C:Superfamily: Y box-binding protein 1; cold shock domain homology
 F:84-148/Domain: cold shock domain homology <CSD>

Query Match 42.5%; Score 742.5; DB 2; Length 291;
 Best Local Similarity 51.0%; Pred. No. 2.9e-38;
 Matches 171; Conservative 16; Mismatches 75; Indels 73; Gaps 9;
 2 SSEATQPPAAPPAALSAADTKPGTTGSGAGS-----GGPGGLTSAAPAGDKKV 54
 18 AADAPAAAPDPAPKSPAAAGAPAPAPALLAGAPARRSPRAPGLISPRGKREKKV 77
 55 IATKVLGTGVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYILRSVGDGETVFDV 114
 78 LATKVLGTGVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYILRSVGDGETVFDV 137
 115 EGEKGAEEAANVTGPGVPGVQGSKYAADRNHYR--YRRRGGPRNYQONTSEGEKNE 172
 138 EGEKGAEEAANVTGPGVPGVQGSKYAADRNHYR--YRRRGGPRNYQONTSEGEKNE 188
 173 GSEAPG-QAQRPPYRRRPPYRRPYGRRPQYNSNPPVQGVVEGADNQAGEOGR 231
 189 MKDGVPEGAQLQVHR-----NPT----- 206
 232 PVQNNYRGYRRFRFRGPPRQRPREDGNEEDKENQDETQGOQPPQRR-YRNNFYRRR 290
 207 -----YRFRFRGPPRPPAPALGEADKENQAANGPNQPSARRGFRFPYNYRR 257
 291 -RPNPKPDGKTKAADPPAENSSAPEAQGGAE 324
 258 PRPLNAVSDGKETKAGEAPTEN-PAPATEQSSAE 291

RESULT 15
 B38274
 Y box-binding protein 2 - African clawed frog
 N:Alternate names: cytoplasmic mRNA-binding protein p54
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 21-Jun-1991 #sequence_revision 21-Jun-1991 #text_change 22-Jun-1999
 C:Accession: B38274; B41786
 R:Tatari, S.R.; Wolffe, A.P.
 Proc. Natl. Acad. Sci. U.S.A. 87, 9028-9032, 1990
 A:Title: Xenopus Y-box transcription factors: molecular cloning, functional analysis, an
 A:Reference number: A38274; MUID:91062413; PMID:12247475
 A:Accession: B38274
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-336 <TAP>
 A:Cross-references: GB:M59454; GB:M38382; NID:G214156; PID:G214157; GB:
 R:Murray, M.T.; Schiller, D.L.; Franke, W.W.
 Proc. Natl. Acad. Sci. U.S.A. 89, 11-15, 1992
 A:Title: Sequence analysis of cytoplasmic mRNA-binding proteins of Xenopus oocytes ident
 A:Reference number: A41786; MUID:92107999; PMID:1729676
 A:Accession: B41786
 A:Molecule type: protein
 A:Residues: 56-82,95-105, 'XXX', 109-113,234-253, 'A', 255 <MUR>
 C:Superfamily: Xenopus Y box-binding protein 2; cold shock domain homology
 C:Keywords: DNA binding; nucleus; oocyte; RNA binding; testis; transcription regulation
 F:44-108/Domain: cold shock domain homology <CSD>

Query Match 36.2%; Score 633; DB 1; Length 336;
 Best Local Similarity 41.8%; Pred. No. 1.5e-31;
 Matches 152; Conservative 43; Mismatches 91; Indels 78; Gaps 11;
 3 SEATQPPAAPPAALSAADTKPGTTGSGAGSGPGGLTSAAPAGDKKVATKVLGT 62

Db	2	SEAEQSEPEVP--QFESEPEIQPG-----IAAARNQANKVLTQVQGT	45
Qy	63	VKWFNVRNGYGFNRNDTKEDVFVHQTAKKNNPRKYLRSVGDGETVEFDVVEGKGAEA	122
Db	46	VKWFNVRNGYGFNRNDTKEDVFVHQTAKKNNPRKFLRSVGDGETVEFDVVEGKGAEA	105
Qy	123	ANVTGPGGVFVQSGKYAADRNHYRR---YPRRRGPPRNTYQNYQNSGEGKNEGSESAPF	179
Db	106	ANVTGPGGVFVQSGRFPAPNRRFRFRFYRPRADTAGESGEGGVSPQMSSEGERGETSPQ	165
Qy	180	GQAQORRRPYRRRPPYMYRRPYGRAPQISNPPVQG-EVMEGADNQ-----GAGE	228
Db	166	QRPQRRRP-----PPFFYRRRRRFRFPNNQNOGAEVTEQSENKDPVAPTSEALASGD	219
Qy	229	Q-----GRPVQNMRYGRFRFRFRGPPRQOPREDGNEEDKENQDGTQOQOPPPQRRYRR	283
Db	220	DPORPPRRRQRRFRFRFR-----PAQQTPEGGDGETKAESGEDPRPE--PQQRNR	272
Qy	284	NFNYYRRR-----PENPKPDGK--ETKAADPPAENS	313
Db	273	PYVQRRRRQGATQVAATAQEGKAEPQHPASEEGTPSDSPTDDGAPVQSSAPDPGIADT	332
Qy	314	SAPF	317
Db	333	PAPE	336

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OM protein - protein search, using sw model

Run on: August 25, 2004, 00:07:24 ; Search time 25 seconds
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674.829 Million cell updates/sec

Title: US-10-028-415-40

Perfect score: 1747

Sequence: 1 MSSEARTQPPAAPAPAL.....AADPPAENSSAPEAEQGGAE 324

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1747	100.0	324	YB1_HUMAN	P16991 h nuclease
2	1707	97.7	322	YB1_MOUSE	P27817 m nuclease
3	1589.5	91.0	301	YB1_CHICK	Q06066 gallus gall
4	1350.5	77.3	303	YB1_XENLA	P21573 xenopus lae
5	1304.5	74.7	305	YB3_XENLA	Q00436 xenopus lae
6	865.5	49.5	361	DBPA_RAT	Q52764 rattus norv
7	840	48.1	372	DBPA_HUMAN	P16989 homo sapien
8	632	36.2	336	YB56_XENLA	P21574 xenopus lae
9	606.5	34.7	324	YB54_XENLA	P45441 xenopus lae
10	497.5	28.5	253	YBPH_APLCA	P41824 aplvia cal
11	186.5	10.7	214	GRP2_NICSY	P27484 nicotiana s
12	178.5	10.2	201	GR2B_ARATH	Q38896 arabidopsis
13	172	9.8	68	CSPE_EUCAI	P57560 buchnera ap
14	172	9.8	68	CSPE_EUCAI	Q89A90 buchnera ap
15	167	9.6	68	CSPC_SHIFL	Q83R19 shigella fl
16	164	9.4	68	CSPE_ECOLI	P36997 escherichia
17	164	9.4	70	CSFG_ECOLI	Q47110 escherichia
18	163	9.3	68	CSFG_ECOLI	P36996 escherichia
19	163	9.3	70	CSFJ_SALTY	P39818 salmonella
20	162.5	9.3	65	CSFC_BACAA	Q45098 bacillus an
21	162	9.3	67	CSFA_MICLU	Q30875 micrococci
22	161	9.2	70	CSF AQAE	Q67327 aquifex aeo
23	160.5	9.2	66	CSFC_BACSU	P39158 bacillus su
24	159.5	9.1	66	CSFA_LISNO	Q48770 listeria mo
25	159	9.1	70	CSFJ_SALTY	P58726 salmonella
26	156	8.9	68	CSFC_EUCAI	P74070 buchnera ap
27	155.5	8.9	2716	CSA DROME	Q81994 drosophila
28	154	8.8	70	CSPE YERPE	Q85593 yersinia pe
29	152.5	8.7	67	CSFA_STRYP	Q34974 streptococc
30	152	8.7	71	CSPE_ECOLI	P36995 escherichia
31	151	8.6	68	CSFA_ECOLI	P72365 stigmatella
32	150	8.6	69	CSFA_ECOLI	P25277 escherichia
33	149.5	8.6	963	YQ36_CABEL	Q09497 caenorhabdi

34	148.5	8.5	356	1	RS41_ARATH	P92966 arabidopsis
35	148	8.5	331	1	PRP1_HUMAN	P04280 homo sapien
36	147	8.4	70	1	CSPV_VIBCH	Q9K116 vibrio chol
37	146	8.4	67	1	CSPF_STRCO	P48859 streptomyce
38	146	8.4	70	1	CSPA_VIBCH	Q9KN00 vibrio chol
39	146	8.4	70	1	CSFG_SHEVI	Q9L170 shewanella
40	145.5	8.3	66	1	CSFB_LISNO	P96791 listeria mo
41	145	8.3	1446	1	IE18_PRVKA	P33479 pseudorabie
42	144.5	8.3	67	1	CSPB_BACSU	P32081 bacillus su
43	143.5	8.2	65	1	CSPB_BACCE	Q45097 bacillus ce
44	143.5	8.2	66	1	CSF THEMA	Q54310 thermotoga
45	143.5	8.2	276	1	PRPL_HUMAN	P10162 homo sapien

ALIGNMENTS

RESULT 1					
YB1_HUMAN					
ID	YB1_HUMAN	STANDARD;	PRP1	324	AA.
AC	P16991; P16990;				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1991 (Rel. 15, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Nuclease sensitive element binding protein 1 (Y box binding protein-1)				
DE	(Y-box transcription factor) (YB-1) (CCAAT-binding transcription				
DE	factor I subunit A) (CBF-A) (Enhancer factor I subunit A) (BFI-A)				
DE	(DNA-binding protein B) (DBPB).				
GN	NSEPI OR YB1.				
OS	Homo sapiens (Human), and				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID:9606, 9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human;				
RX	MEDLINE=89211987; PubMed=2977358;				
RA	Sakura H., Maekawa T., Imamoto F., Yasuda K., Ishii S.;				
RT	"Two human genes isolated by a novel method encode DNA-binding				
RT	proteins containing a common region of homology.";				
RL	Gene 73:499-507(1988).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human;				
RX	MEDLINE=89017190; PubMed=3174636;				
RA	Didier D.K., Schiftenbauer J., Woulfe S.L., Zacheis M., Schwartz B.D.;				
RT	"Characterization of the cDNA encoding a protein binding to the major				
RT	histocompatibility complex class II Y box.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 85:7322-7326(1988).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human; TISSUE=Bone marrow;				
RX	MEDLINE=94245734; PubMed=8188694;				
RA	Horwitz E.M., Maloney K.A., Ley T.J.;				
RT	"A human protein containing a 'cold shock' domain binds specifically				
RT	to H-DNA upstream from the human gamma-globin genes.";				
RL	J. Biol. Chem. 269:14130-14139(1994).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=Human; TISSUE=Kidney, Muscle, and Uterus;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RT	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RT	Altschul S.F., Zeeberg B., Buetow K.H., Bhat N.K.,				
RL	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RN	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RC	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RX	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RT	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gurnaratne P.H.,				
RT	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RL	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				

RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Bovine; TISSUE=Lung endothelial cells;
 RX MEDLINE=93185927; PubMed=844345;
 RA Ozer J., Chakley R., Sealy L.;
 RT "Isolation of the CCAAT transcription factor subunit EF1A cDNA and a
 RT potentially functional EF1A processed pseudogene from Bos taurus:
 RT insights into the evolution of the EF1A/dbpB/YB-1 gene family.";
 RL Gene 124:223-230 (1993).
 CC -!- FUNCTION: Binds to CCAAT-containing Y box of HLA class II genes.
 CC Seems to be a negative regulatory factor.
 CC -!- SUBUNIT: This protein can bind to DNA as a homomeric form, (EPI-
 CC A)n or as a heteromeric form in association with EPI-B. Binds
 CC specifically to H-DNA upstream from the gamma-globin genes.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
 CC
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 CC -----
 CC EMBL; M24070; AAA35750.1; ALT_INIT.
 CC EMBL; J03827; AAA61308.1; -
 CC EMBL; L28809; AAA20871.1; -
 CC EMBL; BC002411; AAH02411.1; -
 CC EMBL; BC010430; AAH10430.1; -
 CC EMBL; BC015208; AAH15208.1; -
 CC EMBL; M95793; AAA30497.1; -
 CC PIR; I39382; I39382.
 CC PIR; JQ2232; JQ2232.
 CC HSSP; P41016; IC90.
 CC TRANSFAC; T00186; -
 CC TRANSFAC; T00910; -
 CC Genew; HGNC:8014; NSEPI.
 CC GK; P16991; -
 CC MIM; 154030; -
 CC GO; GO:0005634; C:nucleus; NAS.
 CC GO; GO:0003677; F:DNA binding; NAS.
 CC GO; GO:0016564; F:transcriptional repressor activity; NAS.
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 CC InterPro; IPR002059; Cold shock.
 CC InterPro; IPR008994; Nucleic_acid_OB.
 CC Pfam; PF00313; CSD; 1.
 CC PRINTS; PF00050; COLDSHOCK.
 CC ProDom; PD00621; Cold_shock; 1.
 CC SMART; SM00357; CSP; 1.
 CC PROSITE; PS00352; COLD_SHOCK; 1.
 KW Transcription regulation; Repressor; DNA-binding; Nuclear protein.
 FT DOMAIN 61 125
 FT CONFLICT 120 120 A -> E (IN REF. 2).
 FT CONFLICT 314 324 SAPEAQGGAE -> BSR (IN REF. 2).
 SQ SEQUENCE 324 AA; 39924 MW; DF0114BF974AEDB8 CRC64;
 Query Match 100.0%; Score 1747; DB 1; Length 324;
 Best Local Similarity 100.0%; Pred. No. 1.3e-100;
 Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSEAEQTPPAAPALSAADTKPTGTGSGAGSGGGLTSAPAGGDKKVIATKVL 60
 DB 1 MSSEAEQTPPAAPALSAADTKPTGTGSGAGSGGGLTSAPAGGDKKVIATKVL 60

QY 61 GTVKFNVNNGVGFNINRNDTKEDVFVHQTAIKKNPKRILSVGDETFVDEVEGEKA 120
 DB 61 GTVKFNVNNGVGFNINRNDTKEDVFVHQTAIKKNPKRILSVGDETFVDEVEGEKA 120
 QY 121 EAANTVGPVGVPVQSGKVAADRNHYRRYPVRRRGGPPRNYQNYQNSSEGEKNGESSEAPEG 180
 DB 121 EAANTVGPVGVPVQSGKVAADRNHYRRYPVRRRGGPPRNYQNYQNSSEGEKNGESSEAPEG 180
 QY 181 QAQORRPVRRRPPPPYMYRRPYGRPPQYNSNPVQGVMEGADNQGAGSQGRPVQRNMYRG 240
 DB 181 QAQORRPVRRRPPPPYMYRRPYGRPPQYNSNPVQGVMEGADNQGAGSQGRPVQRNMYRG 240
 QY 241 YPFRFRPPPRORPREDNEDKENQGDDETOGQOPORRYRRNPNYRRRPNPKPODG 300
 DB 241 YPFRFRPPPRORPREDNEDKENQGDDETOGQOPORRYRRNPNYRRRPNPKPODG 300
 QY 301 KETKAADPPAENSSAPEAQGGAE 324
 DB 301 KETKAADPPAENSSAPEAQGGAE 324
 RESULT 2
 YBI_MOUSE
 ID YBI_MOUSE STANDARD; PRT; 322 AA.
 AC P2781.7; P22569; P43482;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Nuclease sensitive element binding protein 1 (Y box binding protein-1)
 DE (Y-box transcription factor) (YB-1) (CCAAT-binding transcription
 DE factor I subunit A) (CBF-A) (Enhancer factor I subunit A) (EFI-A)
 DE (DNA-binding protein B) (DBPB).
 GN NSEPI OR YB1 OR YBX1 OR MSY-1.
 OS Mus musculus (Mouse), and
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090, 10116;
 RN [1] SEQUENCE FROM N.A.
 RC SPECIES=Mouse; TISSUE=Lens;
 RA Shaughnessy M., Wistow G.J.;
 RT "Absence of MHC expression in lens and cloning of dbpB/YB-1, a DNA-
 RT binding protein expressed in mouse lens.";
 RL Curr. Eye Res. 11:171-181 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse;
 RX MEDLINE=9222631; PubMed=1622927;
 RA Familiari M., Sak D., Wolffe A.P., Tafuri S.R., Ranjan M.;
 RT "The Y-box factors: a family of nucleic acid binding proteins
 RT conserved from Escherichia coli to man.";
 RL New Biol. 4:290-298 (1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse; STRAIN=C57BL/6;
 RX MEDLINE=92158671; PubMed=1741293;
 RA Gai X., Lipson K.E., Prystowsky M.B.;
 RT "Unusual DNA binding characteristics of an in vitro translation
 RT product of the CCAAT binding protein mYB-1.";
 RL Nucleic Acids Res. 20:601-606 (1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse; STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
 RX MEDLINE=92388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shervencko Y., Bouffard G.G., Blakesley A.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Shailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analyses of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
SEQUENCE FROM N.A.
SPECIES=rat; TISSUE=liver;
MEDLINE=91093048; PubMed=1967130;
Ozer J., Faber M., Chalkley R., Sealy L.;
"Isolation and characterization of a cDNA clone for the CCAAT transcription factor EF1A reveals a novel structural motif.";
J. Biol. Chem. 265:22143-22152(1990).
[6]
SEQUENCE FROM N.A.
SPECIES=rat;
Petty K.J., Bartalena L., Nikodem V.M.;
Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE FROM N.A.
SPECIES=rat;
Ogawa H., Date T., Nishizawa M., Pitot H.C., Fujioka M.;
Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Binds to CCAAT-containing Y box of HLA class II genes. Seems to be a negative regulatory factor.
-!- SUBUNIT: This protein can bind to DNA as a homomeric form, (EFI-A)n or as a heteromeric form in association with ERF-B.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.

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EMBL; M50419; AAA40577.1; -
ENBL; M82867; AAA63390.1; -
ENBL; X57621; CAA40847.1; -
ENBL; BC013450; AAH13450.1; -
ENBL; BC013620; AAH13620.1; -
EMBL; M57299; AAA41108.1; -
EMBL; M69138; AAA40906.1; -
EMBL; D13309; BAA02569.1; -
FIR; A23677; A23677.
FIR; I58195; I58195.
HSSP; P41016; IC90.
TRANSFAC; T0235; -
TRANSFAC; T02496; -
MGD; MGI:99146; Nsep1.
InterPro; IPR002059; Cold shock.
InterPro; IPR008994; Nucleic_acid_O3.
Pfam; PF00333; CSD; 1.
PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
SMART; SMC0357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK; 1.
Transcription regulation; Repressor; DNA-binding; Nuclear protein.
DOMAIN 59 123 CSD.
FT CONFLICT 5 5 A -> P (IN REF. 6).
FT CONFLICT 29 29 G -> A (IN REF. 2).
FT CONFLICT 43 45 AAP -> RR (IN REF. 3).
FT CONFLICT 238 238 G -> P (IN REF. 2).
FT

DR Pfam; PF00313; CSD; 1.
 DR PRINTS; PR00050; COLDSHOCK.
 DR PRODOM; PR000621; Cold_shock; 1.
 DR SMART; SM00357; CSP; 1.
 DR PROSITE; PS00352; COLD_SHOCK; 1.
 DR Transcription regulation; Repressor; DNA-binding; Nuclear protein.
 FT DOMAIN 58 122 CSD.
 SQ SEQUENCE 321 AA; 35799 MW; 6496F306C1432274 CRC64;

Query Match 91.0%; Score 1589.5; DB 1; Length 321;
 Best Local Similarity 91.1%; Pred. No. 6e-91;
 Matches 296; Conservative 13; Mismatches 11; Indels 5; Gaps 3;

QY 1 MSSEAEETQPPAAAP-PAAPALSAADTKPGTTGAGSGGPGGLTSAAPAGGDKKVIATKV 59
 DB 1 MSSEAEET-QPPAAAPVPAAPAAADSKP--NGSGNGSGGLASAAPAGGDKKVIATKV 56
 QY 60 LGTVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEGK 119
 DB 57 LGTVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEGK 116
 QY 120 AEAANVTGPGVPGVQSGKYAADRNHYRYPERRGPPPNYQNNYQNSGEGKSGSAP 179
 DB 117 AEAANVTGPGVPGVQSGKYAADRNHYRYPERRGPPPNYQNNYQNSGEGKSGAENIPE 176
 QY 180 GQAQORPYRRRRPPPYMRRPYGRRPYQSNPPVQGEVMEGADNQGAGEQGRPVQRQMYR 239
 DB 177 GQAQORPYRRRRPPPYMRRPYGRRPYQSNPPVQGEVMEGADNQGAGEQGRPVQRQMYR 236
 QY 240 GYRFRFRGPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQ 299
 DB 237 GYRFRFRGPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQ 296
 QY 300 GKETAADPPAENSSAPEAQGGAE 324
 DB 297 GKETAEPPEAENSSAPEAQGGAE 321

RESULT 4
 YB1_XENLA
 ID YB1_XENLA STANDARD; PRT; 303 AA.
 AC P21573;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Nuclease sensitive element binding protein 1 (Y box binding protein-1)
 DE (Y-box transcription factor).
 GN NSEPI OR FRGY1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91062413; PubMed=2247479;
 RA Tafuri S.R., Wolffe A.P.;
 RT "Xenopus Y-box transcription factors: molecular cloning, functional
 analysis and developmental regulation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9028-9032(1990).
 CC -!- FUNCTION: BINDS TO CCAAT-CONTAINING Y BOX OF THE HSP70 GENES.
 CC SEEMS TO BE A NEGATIVE REGULATORY FACTOR.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
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DR EMBL; M59453; A38274; A38274.
 DR PIR; A38274; A38274.
 DR HSSP; P41016; IC90.
 DR TRANSFAC; T00293; -.
 DR InterPro; IPR002059; Cold_shock.
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR Pfam; PF00313; CSD; 1.
 DR PRINTS; PR00050; COLDSHOCK.
 DR PRODOM; PR000621; Cold_shock; 1.
 DR SMART; SM00357; CSP; 1.
 DR PROSITE; PS00352; COLD_SHOCK; 1.
 DR Transcription regulation; Repressor; DNA-binding; Nuclear protein.
 FT DOMAIN 39 103 CSD.
 SQ SEQUENCE 303 AA; 34633 MW; 691E8AB4216137C4 CRC64;

Query Match 77.3%; Score 1350.5; DB 1; Length 303;
 Best Local Similarity 79.7%; Pred. No. 2.5e-76;
 Matches 259; Conservative 9; Mismatches 34; Indels 23; Gaps 3;

QY 1 MSSEAEETQPPAAAPALSAADTKPGTTGAGSGGPGGLTSAAPAGGDKKVIATKV 60
 DB 1 MSSEAEETQ-----QQDALEKAGQ-----EPAATVGDKKVIATKV 38
 QY 61 GTVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEGKA 120
 DB 39 GTVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEGKA 98
 QY 121 EAAANVTGPGVPGVQSGKYAADRNHYRYPERRGPPPNYQNNYQNSGEGKSGSAP 180
 DB 99 EAAANVTGPGVPGVQSGKYAADRNHYRYPERRGPPPNYQNNYQNSGEGKSGSAP 158
 QY 181 -QAQORPYRRRRPPPYMRRPYGRRPYQSNPPVQGEVMEGADNQGAGEQGRPVQRQMYR 239
 DB 159 DDSNQRPYHRRRPPPYMRRPYGRRPYQSNPPVQGEVMEGADNQGAGEQGRPVQRQMYR 218
 QY 240 GYRFRFRGPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQ 299
 DB 219 GYRFRFRGPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQPRQ 278
 QY 300 GKETAADPPAENSSAPEAQGGAE 324
 DB 279 GKETAETSAENTSTPEAQGGAE 303

RESULT 5
 YB3_XENLA
 ID YB3_XENLA STANDARD; PRT; 305 AA.
 AC Q00436;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE B box binding protein (YB3 protein).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=91367675; PubMed=1891365;
 RA Cohen I., Reynolds W.F.;
 RT "The Xenopus YB3 protein binds the B box element of the class III
 promoter.";
 RL Nucleic Acids Res. 19:4753-4759(1991).
 CC -!- FUNCTION: Binds the B box promoter element of genes transcribed
 by RNA polymerase III and is probably involved in the regulation
 of class III genes.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
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```
QY 44 SAAPAG-----GDKVIATKVLGTWKWNVNGYGFINRNDTKEDV 86
Db 59 DAAPATGTAASALAAAGSEAEKKVLTATKVLGTWKWNVNGYGFINRNDTKEDV 118
QY 87 HQTAIKNNPKYLSRGDGETVEFDVVEGEKGAEEAANVTGPGVFPVQGSKYAADRNHYR 146
Db 119 HQTAIKNNPKYLSRGDGETVEFDVVEGEKGAEEAANVTGPGVFPVQGSKYAADRNHYR 178
QY 147 R--YPRRGPRPNYQYNSSEKNEGESAPG-----CAQORRP----- 187
Db 179 RGYGRGRGPRNY-----AGEEEEGSGSEGGFDPATDRQFSGARNQLRRFYRP 230
QY 188 -YRRRRPPYMRPFGRRPQ--YSNPPVQGEVMEGADN--QOAGEQGRPVFQNNMYRGY 241
Db 231 QYQRPRPPHYVGTGTPRSLVPLPHNRIQAGEIGEMKDGVPESQALQG-PVHNN--PTY 287
QY 242 RPRFR-RGPRQRORFEDGNEEDKENQDGTQGGQPPQRR-YRNFNRYRR-RPENPKPQ 298
Db 288 RPYRSRGPFRPPAPAVGEAEDKENQATSGNQPVSRRGYRPPYRNRPRPPNAPSQ 347
QY 299 DGKETKAADPAENSSAPEAQGGAE 324
Db 348 DGKEAKAGEAPTEN-PAPPTQSSAE 372

RESULT 8
YB56_XENLA STANDARD; PRT; 336 AA.
AC P21574;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Cytoplasmic RNA-binding protein p56 (Y box binding protein-2) (Y-box
DE transcription factor) (WRNP4).
GN FRG2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
EN [1]
EN SEQUENCE FROM N.A.
EN MEDLINE=91062415; PubMed=2247479;
RA Tafari S.R., Wolfe A.P.;
RA "Xenopus Y-box transcription factors: molecular cloning, functional
RA analysis and developmental regulation.";
RA Proc. Natl. Acad. Sci. U.S.A. 87:9028-9032(1990).
EN [2]
EN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA MEDLINE=92107999; PubMed=1729676;
RA Murray M.T., Schiller D.L., Franke W.W.;
RA "Sequence analysis of cytoplasmic mRNA-binding proteins of Xenopus
RA oocytes identifies a family of RNA-binding proteins.";
RA Proc. Natl. Acad. Sci. U.S.A. 89:11-15(1992).
EN [3]
EN PARTIAL SEQUENCE.
RC TISSUE=Ovary;
RC MEDLINE=92332467; PubMed=1629179;
RA Deschamps S., Viel A., Garrigos M., Denis H., le Maire M.;
RA "MRNP4, a major mRNA-binding protein from Xenopus oocytes is
RA identical to transcription factor FRG Y2.";
RA J. Biol. Chem. 267:13799-13802(1992).
EN [4]
EN PARTIAL SEQUENCE.
RC TISSUE=Ovary;
RC MEDLINE=91224309; PubMed=1902800;
RA Deschamps S., Viel A., Denis H., le Maire M.;
RA "Purification of two thermostable components of messenger
RA ribonucleoprotein particles (mRNPs) from Xenopus laevis oocytes,
RA belonging to a novel class of RNA-binding proteins.";
RA FEBS Lett. 282:110-114(1991).
CC -!- FUNCTION: Binds to CCAAT-regulatory Y box of the hsp70 genes.
CC Seems to be a negative regulatory factor. Also binds to mRNA.
```

```
CC -!- SUBUNIT: Possibly forms a heterodimer with p54 in the 6S and 15S
CC mRNA-binding particles.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic, either free or associated with
CC ribonucleoprotein particles.
CC -!- TISSUE SPECIFICITY: Testis and immature oocytes.
CC -!- PTM: Phosphorylation activates in vitro RNA-binding.
CC -!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
CC
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CC
CC EMBL; M59454; AA49716.1; -
CC F01; B38274; B38274.
CC HSSP; P41016; IC90.
CC TRANSFAC; T00294; -
CC InterPro; IPR002059; Cold shock.
CC InterPro; IPR006994; Nucleic_acid_OB.
CC Pfam; PF00313; CSD; 1.
CC PRINTS; PR00050; COLDSHOCK.
CC PRODOM; PD000621; Cold_shock; 1.
CC SMART; SM00357; CSP; 1.
CC PROSITE; PS00352; COLD_SHOCK; 1.
CC Transcription regulation; DNA-binding; Nuclear protein;
CC RNA-binding; Phosphorylation.
CC DOMAIN 44 108
CC FT CONFLICT 254 254 A -> T (IN REF. 1).
CC SEQUENCE 336 AA; 37202 MW; 4AD5838769C6B84D CRC64;
SQ
Query Match 36.2%; Score 632; DB 1; Length 336;
Best Local Similarity 41.8%; Pred. No. 3.1e-32;
Matches 152; Conservative 43; Mismatches 91; Indels 78; Gaps 11;
QY 3 SAEATQPPAPAPALSAADTKGTGSGAGSGPGGLTSAAPAGDKKVIATKVLGT 62
Db 2 SEAAQEPFVP--QFSESEPEIQKFG-----IAAARNQANKVLTATQVQGT 45
QY 63 VKWNVNNGYGFINRNDTKEDVFVHOTAIKNNPKYLSRGDGETVEFDVVEGEKGA 122
Db 46 VKWNVNNGYGFINRNDTKEDVFVHOTAIKNNPKYLSRGDGETVEFDVVEGEKGA 105
QY 123 ANVTGPGVFPVQGSKYAADRNHYR---YPRRGPRPNYQYNSSEKNEGESAP 179
Db 106 ANVTGPGVFPVQGSKYAADRNHYR---YPRRGPRPNYQYNSSEKNEGESAP 165
QY 180 GQAQORRPYRRRRFPYMRPFGRRPQYNSPPVQGEVMEGADNQ-----GAGE 228
Db 166 QRPQRRRP-----PPFYRRFRGRPRNNOQGAETGSEKNDPVAPTSEALASGD 219
QY 229 Q-----GRPVQNNMYRGYRFRFRFPFRPRQRPREDGNEEDKENQDGTQGGQPPQRRYR 283
Db 220 DFCRPPFRFRFRFRFRFR-----PAQQTPEGGDGEAKAESGEDPRPE--PQRQRNR 272
QY 284 NFNYRRR-----PENPKPDGK--ETKAADPAENS 313
Db 273 PYVQRRRQGGATQAATAQGEKGAETQHPASEGTPSDPTDDGAPVQSSAPPDGIADT 332
QY 314 SAPE 317
Db 333 PAPE 336

RESULT 9
YB54_XENLA STANDARD; PRT; 324 AA.
ID_YB54_XENLA
AC P4541;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
```


Db 25 EKIIASQVSGTVKFNKSGYGFINDTKEDVHVHQTAVKKNPKYLSVGDGKVE 84
QY 111 FDVVEGKGAEEAANVTGPGVPGVQSGKYAADRNHYR---YPRRGPYPRNYQNYQNS 167
Db 85 FDVVEGKGAEEAANVTGPGVPGVQSGKYAADRNHYRFRAGHYPRFGGRG-----G 135
QY 168 GEXNEGSAPEGAQAQRRPYRRRPPYMYRRPYGRRPOYSNPPVQV---EWMG-ADN 223
Db 136 RPRQMDGAPDFMPS---PRGRGRGPRYYQNR-----RYFGPRRGGGRQYLEGEY 186
QY 224 QGAGEQGRPVQNNYRG---YRPRR---RGPRQ---RQREDGNEEDKENQDQEQ 272
Db 187 QLRDQG---FRGRAPFRVRLRTTSCGLLRRLWLLRPR-----TTQ 227
QY 273 GQPPORRYRRNFYRRRPPENPKPQ 298
Db 228 GRTSQARRRRPWLQPR---QRPKR 251

RESULT 11

GRP2_NICSY
ID GRP2_NICSY STANDARD; PRT; 214 AA.
AC P27484;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE Glycine-rich protein 2.
GN GRP-2.
OS Nicotiana sylvestris (Wood tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=40956;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=92003709; PubMed=1912512;
RX Obokata J., Ohme M., Hayashida N.;
RA "Nucleotide sequence of a cDNA clone encoding a putative glycine-rich
protein of 19.7 kDa in Nicotiana sylvestris.";
RL Plant Mol. Biol. 17:953-955(1991).
CC -!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
CC -!- SIMILARITY: Contains 2 C2HC-type zinc fingers.
CC -!- SIMILARITY: Contains 2 C2HC-type zinc fingers.
CC -!- CAUTION: Was originally (Ref.1) thought to be a cell wall
structural protein.

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CC EMBL; X60007; CAA42622.1; -.
CC PIR; S17731; KNNT2S.
CC HSSP; P15277; IMJC.
CC InterPro; IPR002059; Cold shock.
CC InterPro; IPR008994; Nucleic_acid_OB.
CC InterPro; IPR001878; Znf_CCHC.
CC Pfam; PF00313; CSD; 1.
CC PRINTS; PR00098; zf-CCHC; 2.
CC PRINTS; PR00939; C2HCZNFINGER.
CC PRODOM; PR00050; COLDSHOCK.
CC PRODOM; PR000621; Cold_shock; 1.
CC SMART; SM00357; CSP; 1.
CC SMART; SM00343; Znf_C2HC; 2.
CC PROSITE; PS00352; COLD_SHOCK; 1.
CC PROSITE; PS0158; ZF_CCHC; 2.
KW RNA-binding; Repeat; Zinc-finger.
FT DOMAIN 8 75 CSD.
FT DOMAIN 82 158 GLY-RICH.
FT ZN_FING 157 174 CCHC-TYPE 1.

FT DOMAIN 176 195 GLY-RICH.
FT ZN_FING 194 211 CCHC-TYPE 2.
SQ SEQUENCE 214 AA; 19746 MW; E28DB84538F2A0AA CRC64;
Query Match 10.7%; Score 186.5; DB 1; Length 214;
Best Local Similarity 48.7%; Fred. No. 4e-05; 22; Indels 5; Gaps 2;
Matches 38; Conservative 13; Mismatches 22;
QY 61 GTVKFNVRNGYGFINDTKEDVHVHQTAVKKNPKYLSVGDGKVEFDVVEGK- 119
Db 11 GTVKFNSQKGFITPDGDDLVHQSIRSEG---FRSLAEGTVEFEVSGDGR 66
QY 120 AEAANVTGPGVPGVQSGK 137
Db 67 TKAVDVTGPDGAAVQGR 84

RESULT 12

GR2B_ARATH
ID GR2B_ARATH STANDARD; PRT; 201 AA.
AC Q38896;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Glycine-rich protein 2b (AtGRP2b).
GN GRP2B OR AT2G21060 OR F26H11.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC van Nocker S., Vierstra R.D.;
RA "Arabidopsis AtGRP2b, a glycine-rich protein containing multiple
nucleic acid-binding motifs.";
RL (In) Plant Gene Register PGR95-128.
[2]
SEQUENCE FROM N.A.
RX MEDLINE=20083487; PubMed=16617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umavam L.,
RA Tallon L.J., Gill J.B., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
CC -!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
CC -!- SIMILARITY: Contains 2 C2HC-type zinc fingers.
CC -!- SIMILARITY: Contains 2 CCHC-type zinc fingers.
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CC EMBL; U39072; AAA91165.1; -.
CC EMBL; AC006264; AAD29810.1; -.
CC PIR; F84596; F84596.
CC HSSP; P15277; IMJC.
CC InterPro; IPR002059; Cold shock.
CC InterPro; IPR008994; Nucleic_acid_OB.
CC InterPro; IPR001878; Znf_CCHC.
CC Pfam; PF00313; CSD; 1.


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DR Pfam: PF00098; zf-CCHC; 2.
DR PRINTS; PR00039; C2HCZNFINGER.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold_shock; 1.
DR SMART; SM00357; CSP; 1.
DR SMART; SM00343; ZNF C2HC; 2.
DR PROSITE; PS00352; COLD_SHOCK; 1.
DR PROSITE; PS50158; ZF_CCHC; 2.
KW RNA-binding; Repeat; Zinc-finger.
FT DOMAIN 14 81 CSD.
FT ZN_FING 91 134 GLY-RICH.
FT ZN_FING 136 153 CCHC-TYPE 1.
FT DOMAIN 154 179 GLY-RICH.
FT ZN_FING 180 197 CCHC-TYPE 2.
SQ SEQUENCE 201 AA; 19077 MW; 832411B7FD890E46 CRC64;

Query Match 10.2%; Score 178.5; DB 1; Length 201;
Best Local Similarity 42.2%; Pred. No. 0.00012;
Matches 38; Conservative 18; Mismatches 23; Indels 11; Gaps 3;

QY 48 AGGDKVIATKVLGVKWFVNRNGYGFNRNDTKEDVFVHQTAKKNPKRYLSVGDGE 107
:|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||:
Db 10 SGGRR-----KGVKWFDTQKGFITPSDGGDLFVHQSSIRSEG-----FRSLAAEE 59

QY 108 TVEFDV-VEGEGAAEAANVTSPGGVPVQGS 136
:|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||:
Db 60 SVEFDVVDNSGRPKAIEVSGPDGAPVQGN 89

RESULT 13
CSPE_BUCAI STANDARD; PRT; 68 AA.
AC P57560;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock-like protein cspE (CSP-E).
GN CSPE OR BUSG473.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium), and
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099; 98794;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.a.pisum; STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=1093077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS.";
RL Nature 407:81-86(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.a.graminum;
RX MEDLINE=22084549; PubMed=12089438;
RA Tanas I., Klasson L., Cambaek B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Anderson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC CC -!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
CC CC
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CC -----
DR EMBL; AP001119; BAB13485.1; -.
DR EMBL; AE014123; AAN68016.1; -.

DR HSP; P15277; 1MJC.
DR InterPro; IPR02059; Cold_shock.
DR InterPro; IPR008994; Nucleic_acid_ob.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold_shock; 1.
DR SMART; SM00357; CSP; 1.
DR SMART; SM00357; CSP; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
DR PROSITE; PS50158; ZF_CCHC; 2.
KW Transcription regulation; DNA-binding; Activator; Multigene family;
KW Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 5 65 CSD.
SQ SEQUENCE 68 AA; 7280 MW; 9B57B920CDC6273D CRC64;

Query Match 9.8%; Score 172; DB 1; Length 68;
Best Local Similarity 46.4%; Pred. No. 9.7e-05;
Matches 32; Conservative 14; Mismatches 19; Indels 4; Gaps 1;

QY 57 TKVLGVKWFVNRNGYGFNRNDTKEDVFVHQTAKKNPKRYLSVGDGEVDFVVEG 116
:|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||:
Db 1 SKIKNVKWFNKGFGFITPEDGSKDVFVHFSIQNSG----FKTLAEGQSVFEITEG 56

QY 117 EKGAAANV 125
:|||||:
Db 57 AKGPSAANV 65

RESULT 14
CSPE_BUCBP STANDARD; PRT; 68 AA.
AC Q89A90;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cold shock-like protein cspE (CSP-E).
GN CSPE OR BBP433.
OS Buchnera aphidicola (subsp. Baizongia pistaciae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=135842;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426901; PubMed=12522265;
RA Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
RA Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
RA Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
RT "Reductive genome evolution in Buchnera aphidicola.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC CC -!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
CC CC
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CC -----
DR EMBL; AE014017; AA027142.1; -.
DR InterPro; IPR002059; Cold_shock.
DR InterPro; IPR008994; Nucleic_acid_ob.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR PROSITE; PS00352; COLD_SHOCK; 1.
KW Transcription regulation; DNA-binding; Activator; Multigene family;
KW Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 5 65 CSD.
SQ SEQUENCE 68 AA; 7296 MW; 88768B20CDC6273D CRC64;

Query Match 9.8%; Score 172; DB 1; Length 68;
Best Local Similarity 46.4%; Pred. No. 9.7e-05;

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Query Match          9.6%; Score 167; DB 1; Length 68;
Best Local Similarity 46.4%; Pred. No. 0.0002;
Matches 32; Conservative 14; Mismatches 19; Indels 4; Gaps 1
2y 58 KVLGTWKFNVRNGYGFINRNTKEDVFHQHTAIKKNPKRLSRVSGDGETVEFDVSGE 117
db 2 KIKQWKWFNESHKGFITPDGSKDVFVHPSAIOG-----LKTIAEQNVFEIQGQ 57

118 KGAEAAANVT 126
db 58 KGPAANVT 66

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Search completed: August 25, 2004, 00:24:15
Job time : 27 secs

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.

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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AE015164; AAN43004.1; -.
DR      EMBL; AE016983; AAP16899.1; -.
DR      InterPro; IPR002059; Cold_shock.
DR      Pfam; PF00313; CSD; 1.
DR      PRINTS; PRQ0050; COLDSHOCK.
DR      ProDom; PD006621; Cold_shock; 1.
DR      SMART; SM00357; CSP; 1.
DR      PROSITE; PS00352; COLD_SHOCK; 1.
KW      Transcription regulation; DNA-binding; Activator; Multigene family;
KW      Complete proteome.
KW      INIT MET 0 0 BY SIMILARITY.
FT      DOMAIN 5 65 CSD.
FT      CONFLICT 40 40 L -> F (IN REF. 2.).
SQ      SEQUENCE 68 AA; 7237 MW; EC5D4A4CFAC2EE43 CRC64;

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OM protein - protein search, using sw model

Run on: August 25, 2004, 00:17:20 ; Search time 116 Seconds
(without alignments)
881.275 Million cell updates/sec

Title: US-10-028-415-40
Perfect score: 1747
Sequence: 1 MSSEAEQQPPAAPAPAL.....AADPPAENSAPAEQGGAE 324

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 'SPTEMBL 25':
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	1728	98.9	Q28618 oryctolagus
2	1701	97.4	Q810K5 mus musculus
3	1690	96.7	Q60951 mus musculus
4	1688	96.6	P97752 rattus sp.
5	1626	93.1	Q60950 mus musculus
6	1569	89.8	Q31956 gallus gall
7	1477.5	84.6	Q90376 columba liv
8	1367	78.2	Q8AVK9 xenopus lae
9	1350.5	77.3	Q8AVY9
10	1321	75.6	Q15325 homo sapien
11	1246	71.3	Q08243 gallus gall
12	1133.5	64.9	Q7ZU03 brachydanio
13	1133	64.9	Q93584 brachydanio
14	1110.5	63.6	O13014 carassius a
15	996	57.0	Q8AXS2 oryzias lat
16	876	50.1	Q9N1Q2 canis famli

17	872.5	49.9	361	11	Q80WG4	Q80WG4 mus musculu
18	871.5	49.9	361	11	Q9EQF8	Q9eqf8 mus musculu
19	865.5	49.5	361	11	Q9JKS3	Q9jkb3 mus musculu
20	850.5	48.7	361	11	Q8BP60	Q8bpg0 mus musculu
21	807.5	46.2	263	13	Q90WH2	Q90wh2 flugu rubrip
22	792	45.3	304	6	Q9N1Q3	Q9nlq3 canis famli
23	781	44.7	292	11	Q9EQF7	Q9eqf7 mus musculu
24	753.5	43.1	303	4	Q96B76	Q96b76 homo sapien
25	751	43.0	278	13	Q42232	Q42232 columba liv
26	750.5	43.0	303	4	Q96GD7	Q96gd7 homo sapien
27	713	40.8	298	13	Q90650	Q90650 gallus gall
28	708.5	40.6	308	11	Q61478	Q61478 mus musculu
29	687	39.3	274	11	Q64369	Q64369 mus musculu
30	675.5	38.7	360	11	Q922C8	Q922c8 mus musculu
31	637.5	36.5	364	4	Q8N4P0	Q8n4p0 homo sapien
32	637.5	36.1	364	4	Q9Y2T7	Q9y2t7 homo sapien
33	630.5	36.1	282	11	Q9Z2C7	Q9z2c7 mus musculu
34	620	35.5	199	11	Q9CTJ4	Q9ctt4 mus musculu
35	580.5	33.2	297	13	O13015	O13015 carassius a
36	524.5	30.0	352	5	Q95RE4	Q95re4 drosophila
37	512.5	29.3	317	5	O8IT93	Q8it93 chironomus
38	495	28.3	264	5	O8IT94	Q8it94 chironomus
39	494.5	28.3	342	5	O61580	O61580 drosophila
40	478	27.4	280	5	O86FT3	O86ft3 dugesia etr
41	474.5	27.2	359	5	O46173	O46173 drosophila
42	458.5	26.2	366	13	Q90WH1	Q90wh1 oryzias lat
43	455	26.0	83	11	Q8BRJ5	Q8brj5 mus musculu
44	447	25.6	96	6	Q9XSU1	Q9xsul canis famli
45	424.5	24.3	262	13	Q90676	Q90676 gallus gall

ALIGNMENTS

RESULT 1

Q28618 PRELIMINARY; PRT; 324 AA.

AC Q28618; PRELIMINARY; PRT; 324 AA.

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE P50.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

ON NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;

RX MEDLINE=95155406; PubMed=7852402;

RA Evdokimova V.M., Wei C.L., Sitkov A.S., Simonenko P.N., Lazarev O.A.,

RA Vasilenko K.S., Ustinov V.A., Hershey J.W., Ovchinnikov L.F.;

RT "The major protein of messenger ribonucleoprotein particles in somatic

RT cells is a member of the Y-box binding transcription factor family.";

RL J. Biol. Chem. 270:3186-3192(1995).

CC -I- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.

DR EMBL; U16821; AAA6069.1; -.

DR PIR; A55971; A55971.

DR HSP; P41016; 1C90.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR002059; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR008994; Nucleic_acid_OB.

DR Pfam; PF00313; CSD; 1.

DR PRINTS; PR00050; COLD SHOCK.

DR ProDom; PD000621; Cold shock; 1.

DR SMART; SMC0357; CSP; 1.

DR PROSITE; PS00352; COLD SHOCK; 1.

SQ SEQUENCE 324 AA; 35824 MW; B2700FD2E61BF8B9 CRC64;

Query Match 98.9%; Score 1728; DB 6; Length 324;
Best local Similarity 98.8%; Pred. No. 1.8e-122;
Matches 320; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

P97752 PRELIMINARY; PRT; 322 AA.
AC P97752; 1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TSH receptor suppressor element-binding protein-1.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96435261; PubMed=8838147;
RA Omori M., Shimura H., Shimura Y., Kohn L.D.;
RT "A Y-box protein is a suppressor factor that decreases thyrotropin
RT receptor gene expression.";
RL Mol. Endocrinol. 10:78-89 (1996).
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; S83025; AAB46889.2; -.
DR HSP; P41016; 1C90.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008994; Cold shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold shock; 1.
DR SMART; SM00357; CSP; 1-
DR PROSITE; PS00352; COLD_SHOCK; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35531 MW; DD6682F62F11D4A8 CRC64;

Query Match 96.6%; Score 1688; DB 11; Length 322;
Best Local Similarity 97.5%; Pred. No. 1.9e-119;
Matches 316; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 1 MSSAEATQPPAAPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKIATKVL 60
Db 1 MSSAEATQPPAAP--AAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGGDKKIATKVL 58

Qy 61 GTVKWNVNRYGFINRNDTKEDVFVHQTAKNNPKYLSVGDGTFVDFVVEGEKGA 120
Db 59 GTVKWNVNRYGFINRNDTKEDVFVHQTAKNNPKYLSVGDGTFVDFVVEGEKGA 118

Qy 121 EAAVNTGPGGVQGVQSKYAADRNNHYRRYRRRRGPPRNYQNYQNSSEKESGSAPEG 180
Db 119 EAAVNTGPGGVQGVQSKYAADRNNHYRRYRRRRGPPRNYQNYQNSSEKESGSAPEG 178

Qy 181 QAQQRPRRRRPPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRR 240
Db 179 QAQQRPRRRRPPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRR 238

Qy 241 YRPRFRGPPRQPRPDGNEEDKENQDGTQGGQPPQRRYRRNFRNFRNFRNFRNFRNFRNFRN 300
Db 239 YRPRFRGPPRQPRPDGNEEDKENQDGTQGGQPPQRRYRRNFRNFRNFRNFRNFRNFRNFRN 298

Qy 301 KETKAADPPAENSAPAEQGGAE 324
Db 299 KETKAADPPAENSAPAEQGGAE 322

RESULT 5
Q60950 PRELIMINARY; PRT; 322 AA.
AC Q60950;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MYB-1a.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57 Black/6 X CBA; TISSUE=Thymus;
RA Schwartz B.D., Meador J.W. III, Wolfe S.L.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; U33196; AAA75475.1; -.
DR HSP; P41016; 1C90.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002059; Cold shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold shock; 1.
DR SMART; SM00357; CSP; 1-
DR PROSITE; PS00352; COLD_SHOCK; 1.
SQ SEQUENCE 322 AA; 36007 MW; E4E96AF7924544DA CRC64;

Query Match 93.1%; Score 1626; DB 11; Length 322;
Best Local Similarity 94.4%; Pred. No. 8.9e-115;
Matches 306; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

Qy 1 MSSAEATQPPAAPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKIATKVL 60
Db 1 MSSAEATQPPAAP--AAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGGDKKIATKVL 58

Qy 61 GTVKWNVNRYGFINRNDTKEDVFVHQTAKNNPKYLSVGDGTFVDFVVEGEKGA 120
Db 59 GTVKWNVNRYGFINRNDTKEDVFVHQTAKNNPKYLSVGDGTFVDFVVEGEKGA 118

Qy 121 EAAVNTGPGGVQGVQSKYAADRNNHYRRYRRRRGPPRNYQNYQNSSEKESGSAPEG 180
Db 119 EAAVNTGPGGVQGVQSKYAADRNNHYRRYRRRRGPPRNYQNYQNSSEKESGSAPEG 178

Qy 181 QAQQRPRRRRPPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRR 240
Db 179 QAQQRPRRRRPPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRRPYRR 238

Qy 241 YRPRFRGPPRQPRPDGNEEDKENQDGTQGGQPPQRRYRRNFRNFRNFRNFRNFRNFRNFRN 300
Db 239 YRPRFRGPPRQPRPDGNEEDKENQDGTQGGQPPQRRYRRNFRNFRNFRNFRNFRNFRNFRN 298

Qy 301 KETKAADPPAENSAPAEQGGAE 324
Db 299 KETKAADPPAENSAPAEQGGAE 322

RESULT 6
Q91956 PRELIMINARY; PRT; 326 AA.
AC Q91956;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mouse dbpB/VB-1 protein homologue, clone CLFEST34.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lens fibers;
RA MEDLINE=96437509; PubMed=8840185;
RA Sawada K., Agata K., Eguchi G.;
RT "Characterization of terminally differentiated cell state by
RT categorizing cDNA clones derived from chicken lens fibers.";
RL Int. J. Dev. Biol. 40:531-535 (1996).
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; D26328; BAA05380.1; -.

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DR HSP; P41016; 1C90.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002059; Cold shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold shock; 1.
DR SMART; SM00357; CSP; 1_shock; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
SQ SEQUENCE 326 AA; 36319 MW; F49E5FFACFD9D447 CRC64;

Query Match      89.8%; Score 1569; DB 13; Length 326;
Best Local Similarity 89.4%; Pred. No. 1.8e-110;
Matches 295; Conservative 13; Mismatches 12; Indels 10; Gaps 4;

QY 1 MSSEAETQPPAA--PPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKIATK 58
DB 1 MSSEAET-QPPAAFPVPAAPAAADNSHYRRYPRRRGPPRNYQNYQNSSEGEKNEGAENIP 56

QY 59 VLGTWKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEK 118
DB 57 VLGTWKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEK 116

QY 119 GAEEAANTGPGGVVQSGKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSAP 178
DB 117 GAEEAANTGPGGVVQSGKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGAENIP 176

QY 179 EGQAQQRREYRRRRFPYVYRRPGRPOYSNPVQGVMEGADNQGAGGQGRPVQNNMY 238
DB 177 EGQAQQRREYRRRRFPYVYRRPGRPOYSNPVQGVMEGADNQGAGGQGRPVQNNMY 236

QY 239 RGYRPRFR---RGPPRQRPREDGNEEDKENQDGTQGOQPPQRRYRNFYRRRPN 294
DB 237 RGYRPRFRSLTFRGPPRQRPREDGNEEDKENQDGTQGOQPPQRRYRNFYRRRPN 296

QY 295 KPQDQKTKAADPPAENSAPEAQGGAE 324
DB 297 KPQDQKTKTAEPPEAENSAPEAQGGAE 326

RESULT 7
ID Q90376 PRELIMINARY; PRT; 287 AA.
AC Q90376;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Y-box binding protein.
GN PYBALPHA.
OS Columbia livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Roller;
RA Pratt S.L., Horseman N.D.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; U43513; AAB01787.1; -.
DR HSP; P41016; 1C90.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002059; Cold shock.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR Pfam; PF00313; CSD; 1.
DR ProDom; PD000621; Cold shock; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR SMART; SM00357; CSP; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
SQ SEQUENCE 287 AA; 32363 MW; 1770B83E824A0B35 CRC64;

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Query Match      84.6%; Score 1477.5; DB 13; Length 287;
Best Local Similarity 84.6%; Pred. No. 1.2e-103;
Matches 274; Conservative 8; Mismatches 5; Indels 37; Gaps 1;

QY 1 MSSEAETQPPAAFPAPALSAADTKPGTTGSGAGSGGPGGLTGAAPAGGDKKIATKVL 60
DB 1 MSSEAETQ-----PPAGGDKKIATKVL 23

QY 61 GTVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 120
DB 24 GTVKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEKGA 83

QY 121 EAANTGPGGVVQSGKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSAP 180
DB 84 EAANTGPGGVVQSGKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGAENIP 143

QY 181 QAQQRPRYRRRRFPYVYRRPGRPOYSNPVQGVMEGADNQGAGGQGRPVQNNMYRG 240
DB 144 QAQQRPRYRRRRFPYVYRRPGRPOYSNPVQGVMEGADNQGAGGQGRPVQNNMYRG 203

QY 241 YPRFRRRGPPROROPREDGNEEDKENQDGTQGOQPPQRRYRNFYRRRPNPKPDG 300
DB 204 YPRFRRRGPPROROPREDGNEEDKENQDGTQGOQPPQRRYRNFYRRRPNPKPDG 263

QY 301 KETKAADPPAENSAPEAQGGAE 324
DB 264 KETKAEPPEAENSAPEAQGGAE 287

RESULT 8
QYAVK9 PRELIMINARY; PRT; 304 AA.
ID Q8AVK9
AC Q8AVK9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to nuclease sensitive element binding protein 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042217; AAH42217.1; -.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002059; Cold shock.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold shock; 1.
DR SMART; SM00357; CSP; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
SQ SEQUENCE 304 AA; 34390 MW; 085C185E4813129E CRC64;

Query Match      78.2%; Score 1367; DB 13; Length 304;
Best Local Similarity 80.8%; Pred. No. 2.8e-95;
Matches 265; Conservative 13; Mismatches 22; Indels 28; Gaps 5;

QY 1 MSSEAET-QPPAAFPAPALSAADTKPGTTGSGAGSGGPGGLTGAAPAGGDKKIATK 58
DB 1 MSSEVETQEQPDAL-----GKAGQEPAAV-GEKKIATK 36

QY 59 VLGTWKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEK 118
DB 37 VLGTWKFNVRNGYGFINRNDTKEDVFVHQTAKKNNPKYLSVGDGETVEFDVVEGEK 96

QY 119 GAEEAANTGPGGVVQSGKYAADRNHYRRYPRRRGPPRNYQNYQNSSEGEKNEGSAP 178

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DB 118 EAAVTGGVPGVQSGKYAADRNHYRRYPRRRGPRNYQQYQNSGEKNESESAPAE 177
QY 181 QAOQRPRYRRRFPYPPYMRGRRPOYSNPPVOGEVMEGADNOGAGEQGRPVQRNMYRG 240
DB 178 RPNNAAY-AGEVETLLHAETVLLHAETVLLHAETVLLHAETVLLHAETVLLHAET 236
QY 241 YRPRFRGPPRRQPRREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNFRNFRNFRN 300
DB 237 IDHDSAGALLAKROFREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNFRNFRNFRN 296
QY 301 KETKAADPPAENSAPAEQSGAE 324
DB 297 KETKAADPPAENSAPAEQSGAE 320

RESULT 11
Q08243 PRELIMINARY; PRT; 348 AA.
AC Q08243;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE CCAAT-binding protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94120725; PubMed=8291233;
RA Kandala J.C., Guntaka R.V.;
RT "Cloning of Rous sarcoma virus enhancer factor genes. I. Evidence that
RT RSV-EF-1 is related to Y-box (inverted CCAAT) binding proteins and
RT binds to multiple motifs in the RSV enhancer."
RL Virology 198;1514-523(1994).
CC -!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; L20500; AAA18017.1; -.
DR PIR; A49594; A49594.
DR HSP; P41016; ICD0.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000028; Chloroperoxidase.
DR InterPro; IPR002059; Cold shock.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR Pfam; PF00313; CSD; 1.
DR ProDom; PD000621; Cold shock; 1.
DR SMART; SMC0357; CSP; 1.
FT NON TER 1
SQ SEQUENCE 348 AA; 39405 MW; 4795EA2007ED062F CRC64;

Query Match 71.3%; Score 1246; DB 13; Length 348;
Best Local Similarity 75.0%; Pred. No. 4.5e-86;
Matches 243; Conservative 15; Mismatches 48; Indels 18; Gaps 4;

QY 5 AETQPP-----PAAPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATK 58
DB 4 AETQPPAAPVPAPPPPPPTTNTLTA-----ACTGAAMPRLRLRERGQEGH-----RNE 52
QY 59 VLGTWKFVNRNGYGFINRNDTKEDVFVHQTAKKQNPRLRSVGDGTETVDFVVEGK 118
DB 53 GFGNSEMVNRNGYGLMNRNDTKEDVFVHQTAKKQNPRLRSVGDGTETVDFVVEGK 112
QY 119 GAAANVTGPGVPGVQSGKYAADRNHYRRYPRRRGPRNYQQYQNSGEKNESESAP 178
DB 113 GAAANVTGPGVPGVQSGKYAADRNHYRRYPRRRGPRNYQQYQNSGEKNESESAP 172
QY 179 EGOAQRPRYRRRFPYPPYMRGRRPOYSNPPVOGEVMEGADNOGAGEQGRPVQRNMYRG 238
DB 173 EGOAQRPRYRRRFPYPPYMRGRRPOYSNAPVQGEIVGADNOGAGEQGRPVQRNMYRG 231
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QY 239 RGYRFRFRGPPRRQPRREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNFRNFRNFRN 298
DB 232 RGYRFRFRGPPRRQPRREDGNEEDKENQDGTQGGQPPQRRYRNFNFRNFRNFRNFRN 291
QY 299 DCKETKAADPPAENSAPAEQSG 322
DB 292 DCKETKAADPPAENSAPAEQSG 315

RESULT 12
Q7ZU03 PRELIMINARY; PRT; 309 AA.
AC Q7ZU03;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Nuclease sensitive element binding protein 1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalot D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smutts D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Body;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC050156; AAH50156.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002059; Cold shock.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold shock; 1.
DR SMART; SM00357; CSP; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
SQ SEQUENCE 309 AA; 34935 MW; 7CF1CCFE7DF5777A CRC64;

Query Match 64.9%; Score 1133.5; DB 13; Length 309;
Best Local Similarity 69.6%; Pred. No. 1.2e-77;
Matches 233; Conservative 26; Mismatches 39; Indels 37; Gaps 11;

QY 1 MSSAEATQPPAAPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
DB 1 MSSAEATQPPAAPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 40
QY 61 GTVWFVNRNGYGFINRNDTKEDVFVHQTAKKQNPRLRSVGDGTETVDFVVEGK 120
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Db 41 GTVKWNVNRYGFIINRNDTKEDVFHQTAIKKNPRKYLRSVGDGETVEFDVVEGEKA 100
QY 121 EAAVNTGPGGVPVQGSKYAADRNHYRRYPRRRGPPRNYQNYQN---SESGEKNEGESA 177
Db 101 EAAVNTGPGGVPVQGSKYAADRNHYRRYPRRRGPPRNYQNYQSDPEABPREKREGAESA 160
QY 178 PEG--QAQORRPY--RRRRPPPYMRPPYGRRRPOYSNPPVQGVMEGA---DNQAGEQG 230
Db 161 PEGEMOQQQRPTYPGRRRYPYFVRRYRGRPPYTNQ-RGEMTEGGGEEENQGGPDQG 219
QY 231 -RPVRQNMRYGRYPRRRGPPRQRPREDGNEEDKENQGDGTQGGQPPQRRYRNFNRYR 289
Db 220 NKPWRQNYRGFRP--RGPPRR--PVRDG-EEDKENQSGQNPQRRYRNFNRYR 274
QY 290 RRPENPKQDGKTKAADPPAENSAPAEBOGGAE 324
Db 275 RRPQTTKPDGKDSKAADASADKSAAPAEBOGGAD 309
RESULT 13
O93584 PRELIMINARY; PRT; 310 AA.
AC O93584;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Zfy1.
GN NSEPI.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99376608; PubMed=10446383;
RA Chang B.E., Lin C.Y., Kuo C.M.;
RT "Molecular cloning of a cold-shock domain protein, zfy1, in zebrafish
embryo."
EL Biochim. Biophys. Acta 1433:343-349 (1999).
CC DR EMBL; AF093129; AAC62774.1; -.
DR ZFIN; ZDB-GENE-000629-3; nsepi.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002059; Cold shock
DR InterPro; IPR008994; Nucleic_acid_OB.
DR Pfam; PF00313; CSD; 1.
DR ProDom; PD000621; Cold shock; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR SMART; SM00357; CSP; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
SQ SEQUENCE 310 AA; 35022 MW; 64430D39DD56D0DE CRC64;
Query Match 64.9%; Score 1133; DB 13; Length 310;
Best Local Similarity 69.6%; Pred. No. 1.3e-77;
Matches 233; Conservative 26; Mismatches 40; Indels 36; Gaps 11;
QY 1 MSSAEATQPPAAPPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
Db 1 MSSAEATQPP--QFADAESFS-----PAAATAGDKKVIATKVL 40
QY 61 GTVKWNVNRYGFIINRNDTKEDVFHQTAIKKNPRKYLRSVGDGETVEFDVVEGEKA 120
Db 41 GTVKWNVNRYGFIINRNDTKEDVFHQTAIKKNPRKYLRSVGDGETVEFDVVEGEKA 100
QY 121 EAAVNTGPGGVPVQGSKYAADRNHYRRYPRRRGPPRNYQNYQN---SESGEKNEGESA 177
Db 101 EAAVNTGPGGVPVQGSKYAADRNHYRRYPRRRGPPRNYQNYQSDPEABPREKREGAESA 160
QY 178 PEG--QAQORRPY--RRRRPPPYMRPPYGRRRPOYSNPPVQGVMEGA---DNQAGEQG 230
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Db 161 PEGEMOQQQRPTYPGRRRYPYFVRRYRGRPPYTNQ-RGEMTEGGGEEENQGGPDQG 219
QY 231 -RPVRQNMRYGRYPRRRGPPRQRPREDGNEEDKENQGDGTQGGQPPQRRYRNFNRYR 289
Db 220 NKPWRQNYRGFRP--SRGPPRR--PVRDG-EEDKENQSGQNPQRRYRNFNRYR 275
QY 290 RRPENPKQDGKTKAADPPAENSAPAEBOGGAE 324
Db 275 RRPQTTKPDGKDSKAADASADKSAAPAEBOGGAD 310
RESULT 14
O13014 PRELIMINARY; PRT; 311 AA.
AC O13014;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Y box protein 1.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98055714; PubMed=9395336;
RA Katsu Y., Yamashita M., Nagahama Y.;
RT "Isolation and characterization of goldfish Y box protein, a germ-
cell-specific RNA-binding protein."
RL Eur. J. Biochem. 249:854-861 (1997).
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; AB003335; BAA19849.1; -.
DR HSP; P41016; 1C90.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002059; Cold shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold shock; 1.
DR SMART; SM00357; CSP; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
SQ SEQUENCE 311 AA; 35076 MW; 3611B8F4E5914039 CRC64;
Query Match 63.6%; Score 1110.5; DB 13; Length 311;
Best Local Similarity 68.5%; Pred. No. 6.5e-76;
Matches 228; Conservative 24; Mismatches 50; Indels 31; Gaps 8;
QY 1 MSSAEATQPPAAPPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGDKKVIATKVL 60
Db 1 MSSAEATQPP--QFAADAES-----PSSPSPAATAGDKKVIATKVL 41
QY 61 GTVKWNVNRYGFIINRNDTKEDVFHQTAIKKNPRKYLRSVGDGETVEFDVVEGEKA 120
Db 42 GTVKWNVNRYGFIINRNDTKEDVFHQTAIKKNPRKYLRSVGDGETVEFDVVEGEKA 101
QY 121 EAAVNTGPGGVPVQGSKYAADRNHYRRYPRRRGPPRNYQNYQ--NSEGEKNEGESAPE 179
Db 102 EAAVNTGPGGVPVQGSKYAADRNHYRRYPRRRGPPRNYQNYQSDPEABPREKREBENAPE 161
QY 180 G--QAQORRPY--RRRRPPPYMRPPYGRRRPOYSNPPVQGVMEGA---DNQAGEQG-R 231
Db 162 GEMQPOORLPTTPGRRRYPYFVRRYRGRPPYTNAPQEGEMPEGEGENQGVPDQGNK 221
QY 232 PVRQNMRYGRYPRRRGPPRQRPREDGNEEDKENQGDGTQGGQPPQRRYRNFNRYR 291
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Db 222 PMRQNYRFGFGP---RGLPRPRVREGEEKEKQGGQNGQEPFCRCYRRNFYRRR 278
Qy 292 PENPKPDQKTKAADPPAENSSAPAEAGGAE 324
Db 279 PÖTKLODGDGSKAADASADKPAAPAEAGGAE 311

RESULT 15

Q8AXS2

ID Q8AXS2 PRELIMINARY; PRT: 306 AA.

AC Q8AXS2;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Y-box binding protein.

GN YB1

OS Oryzias latipes (Medaka fish) (Japanese ricefish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

OX NCBI_TaxID=8090;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohe N.;

RT "Cloning of Japanese Medaka Y-box binding protein cDNA";

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RE EMBL; AB041646; BAC45236.1; -.

DR GO: 0003677; F:DNA binding; IEA.

DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR02059; Cold_shock.

DR InterPro: IPR008994; Nucleic_acid_OB.

DR Pfam: PF00313; CSD; 1.

DR PRINTS: PR00050; COLDSHOCK.

DR PRODom: PD00621; Cold shock; 1.

DR SMART: SM00357; CSP; 1.

DR PROSITE: PS00352; COLD_SHOCK; 1.

SQ SEQUENCE 306 AA; 33718 MW; 5244E7EC94D41696 CRC64;

Query Match

Best Local Similarity 57.0%; Score 996; DB 13; Length 306;

Matches 219; Conservative 19; Mismatches 47; Indels 60; Gaps 14;

Qy 1 MSSEATQOPPAAPPAALSAADTKPTGSGAGSGPGGLTSAAPAGDKKVIATKVL 60

Db 1 MSSEATQOPPAAPPAALSAADTKPTGSGAGSGPGGLTSAAPAGDKKVIATKVL 42

Qy 61 GTVAKFNVNRNGYGFINEKEDVVFHQTAIKNNPKYLSVGDGETVEFDVVEGEKA 120

Db 43 GTVAKFNVNRNGYGFINEKEDVVFHQTAIKNNPKYLSVGDGETVEFDVVEGEKA 102

Qy 121 EAAVNTGPGVPGVGSYAADRNHYRRYRRRPPR--NYQNYQNSESGE----- 169

Db 103 EAAVNTGPGVAVGGSYAADRNHYRRYRRRPPRPGGEYPENYPSDGEPCGNGVRDKG 162

Qy 170 KNEGESAPEG--QAQORRPY--RRRRFPYMRYPYRRFPQYNSFPVQGEVMEGADNOG 225

Db 163 NRDGESAPEGEQPQORRTYPSRRYPYP-----GVEGDENOG 203

Qy 226 AGEQG-RPVQNNMYRGVRRFR-RGPPRQRPREDGNEEDKENQGDDE-TGQQPPQRRYR 282

Db 204 GPDQGNKPVQNYRGVRRFTRPRGPPRR-PVRDG-EEDKENQGGGQNGQPPQRRYR 261

Qy 283 RNFNRYRRRPE-NPKP-ODGKETKA-ADPPAENSSAPAEAGGAE 324

Db 262 RNFNRYRRROQTGKPGQESKADAKAGEPSAEKTSAPAEAGGAE 306

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Job time : 121 secs